

Glu Pro Thr Ser His Gln Thr Ser Leu Phe Gly Tyr Ala Val Asn Ser
20 25 30

Ser Leu Ala Thr Thr Asn Ala Ala Ser Leu Leu Gly Val Ala Asn Asp
35 40 45

Ala Gly Leu Leu Ala Ala Arg Val Tyr Pro Gly Val Tyr Val Gln Gly
50 55 60

Pro Ser Gly Gln Met Ile Pro Asn Thr Asp Leu Ala Ser Thr Gln Val
65 70 75 80

Leu Pro Gly Ile Asn Arg Gln Val Ile Tyr Thr Ile Asn Glu Asp Ala
85 90 95

Thr Tyr Ser Asp Gly Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser
100 105 110

Ala Thr Ala Gly Gln Met Pro Glu Leu Phe Gln Ser His Val Pro Leu
115 120 125

Thr Ser Gln Ile Glu Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala
130 135 140

Thr Val Val Phe Lys Glu Asp Leu Gly Glu Arg Trp Arg Tyr Leu Phe
145 150 155 160

Glu Gln Gly Asp Leu Leu Pro Ala His Ala Val Ala Ser Lys Ala Gly
165 170 175

Met Thr Leu Glu Glu Leu Asn Gln Ala Leu Lys Asp Lys Asp Pro Glu
180 185 190

Ala Leu Thr Glu Pro Ala Arg Val Trp Ser Glu Gly Phe Gln Leu Ser
195 200 205

Gln Phe Asp Pro Glu Leu Gln Thr Ala Phe Gly Pro Tyr Lys Val Asp
210 215 220

Ser Val Gly Glu Phe Gly Glu Val Lys Leu Val Arg Asn Glu Phe Tyr
225 230 235 240

Ser Gly Asp Gln Ala Val Glu Ala Glu Ile Thr Met Trp Pro Lys Gly
245 250 255

Ser Asp Leu Ser Ala Ile Ala Asp Asn Gly Asn Leu Gln Ile Ala His
260 265 270

Val Val Ala Trp Glu Ser Glu Pro Trp Val Asn Arg Asp Asp Pro Leu
275 280 285

Asn Pro Tyr Asp Ile Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu
290 295 300

Thr Leu Ala Ser Ala Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala
305 310 315 320

Phe Ala Ala Cys Val Asp Gln Glu Ala Val Ala Ala Ser Ser Ser
325 330 335

Ile Ser Gly Ile Asp Val Pro Ala Val Gly Val His Ser Val Arg His
 340 345 350

Gln Asn Pro Val Val His Gln Ile Gly Asp Leu Pro Ala Gln His Met
 355 360 365

Ala Val Asp Ile Asn Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg
 370 375 380

Ile Gly Tyr Asp Gly Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala
 385 390 395 400

Ile Arg Gln Ser Cys Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser
 405 410 415

Gln Glu Ala Val Ser Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu
 420 425 430

Trp Gly Tyr Glu Gln Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg
 435 440 445

Thr Val Asp Pro His Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr
 450 455 460

Asp Ala Glu Ser Thr Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val
 465 470 475 480

Pro Ser Ile Pro Leu Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg
 485 490 495

Thr Val Gly Asn Val Val Val Asn Thr Asp Leu Ala Gly Ile Gly Trp
 500 505 510

Asn Met Asp Arg Trp Ser Arg Ser Glu Glu
 515 520

<210> 1101

<211> 408

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(385)

<223> RXC02238

<400> 1101

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ctcttaaacac tactgtccat atactttga aaagggtgtca gtg acc aac gtg agc 115
 Val Thr Asn Val Ser
 1 5

aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163
 Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile
 10 15 20

acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211
 Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr
 25 30 35

gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe	259
40 45 50	
tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val	307
55 60 65	
act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile	355
70 75 80 85	
aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca Asn Ala Gly Leu Leu Asp His Glu Glu Gly	405
90 95	
cac	408

<210> 1102

<211> 95

<212> PRT

<213> Corynebacterium glutamicum

<400> 1102

Val Thr Asn Val Ser Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp
1 5 10 15Pro Pro Val Gly Ile Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys
20 25 30Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg
35 40 45Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe
50 55 60Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile
65 70 75 80Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly
85 90 95

<210> 1103

<211> 1298

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1275)

<223> RXC01946

<400> 1103

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Ile Arg Lys Tyr Ser Arg Leu Glu Glu Gln Phe Gln Ser Leu Gly Gly
1 5 10 15

tac gaa gct gac gcc gaa gca gcc cag atc tgc gac aac ctc ggc ctc 96

Tyr Glu Ala Asp Ala Glu Ala Ala Gln Ile Cys Asp Asn Leu Gly Leu			
20	25	30	
gag gca cgc atc ctc gac cag cag ctt aaa acc ctg tcc ggc ggc cag			144
Glu Ala Arg Ile Leu Asp Gln Gln Leu Lys Thr Leu Ser Gly Gly Gln			
35	40	45	
cgc cgc cgc gtc gag ttg gcg cag atc ctc ttc gcc gcc acc aac ggc			192
Arg Arg Arg Val Glu Leu Ala Gln Ile Leu Phe Ala Ala Thr Asn Gly			
50	55	60	
tcc ggc aaa tca aaa acc aca ttg ctt ctc gac gag ccc acc aac cac			240
Ser Gly Lys Ser Lys Thr Thr Leu Leu Leu Asp Glu Pro Thr Asn His			
65	70	75	80
ttg gac gca gac tcg atc acc tgg ctc cgt gac ttc ctg gcg aag cac			288
Leu Asp Ala Asp Ser Ile Thr Trp Leu Arg Asp Phe Leu Ala Lys His			
85	90	95	
gaa ggt gga ctg atc atg att tcg cac gac gtc gaa ctg ctt ggc gcc			336
Glu Gly Gly Leu Ile Met Ile Ser His Asp Val Glu Leu Leu Gly Ala			
100	105	110	
gta tgt aac aag att tgg tac ctc gac gca gta cgc agc gaa gcc gat			384
Val Cys Asn Lys Ile Trp Tyr Leu Asp Ala Val Arg Ser Glu Ala Asp			
115	120	125	
gtc tac aac atg ggc ttt agc aaa tac gtc gat gca cgt gca ctc gat			432
Val Tyr Asn Met Gly Phe Ser Lys Tyr Val Asp Ala Arg Ala Leu Asp			
130	135	140	
gaa gca cgc cga cgc cgt gag cgc gca aac gcc gaa aag aag gcc gga			480
Glu Ala Arg Arg Arg Glu Arg Ala Asn Ala Glu Lys Lys Ala Gly			
145	150	155	160
gcc ctc aag gac cag gct gca cgc ctc ggc gcg aaa gca acc aag gct			528
Ala Leu Lys Asp Gln Ala Ala Arg Leu Gly Ala Lys Ala Thr Lys Ala			
165	170	175	
gcc gca gct aag cag atg atc gcc cgt gcg gaa cga atg atc gac aac			576
Ala Ala Ala Lys Gln Met Ile Ala Arg Ala Glu Arg Met Ile Asp Asn			
180	185	190	
ctc gac gaa atc cgc gta gct gac cgc gcc aac atc gtt ttc cca			624
Leu Asp Glu Ile Arg Val Ala Asp Arg Ala Ala Asn Ile Val Phe Pro			
195	200	205	
gaa cca gca ccc tgt gga aaa acc cca ctc aac gcc aag ggc ctg acc			672
Glu Pro Ala Pro Cys Gly Lys Thr Pro Leu Asn Ala Lys Gly Leu Thr			
210	215	220	
aag atg tac ggc tcc ctc gaa gtc ttc gcc ggc gtc gac cta gcc atc			720
Lys Met Tyr Gly Ser Leu Glu Val Phe Ala Gly Val Asp Leu Ala Ile			
225	230	235	240
gac aaa ggc tcc cgc gta gtc gtc ctc gga ttc aac ggt gca ggt aaa			768
Asp Lys Gly Ser Arg Val Val Leu Gly Phe Asn Gly Ala Gly Lys			
245	250	255	
acc acc ctc ctc aaa ctc ctc gcc ggt gtg gaa cgc acc gac ggc gaa			816
Thr Thr Leu Leu Lys Leu Leu Ala Gly Val Glu Arg Thr Asp Gly Glu			

260	265	270	
ggc ggc atc gtc acc gga tac ggc ctc aaa atc ggc tac ttc gcc cag Gly Gly Ile Val Thr Gly Tyr Gly Leu Lys Ile Gly Tyr Phe Ala Gln 275 280 285 864			
gaa cac gac acc atc gac ccc gac aaa tcc gtc tgg caa aac acc atc Glu His Asp Thr Ile Asp Pro Asp Lys Ser Val Trp Gln Asn Thr Ile 290 295 300 912			
gaa gcc tgc gcc gac gcc gac caa caa agc ctc cgc agc ctc ctc gga Glu Ala Cys Ala Asp Ala Asp Gln Gln Ser Leu Arg Ser Leu Leu Gly 305 310 315 320 960			
tcc ttc atg ttc tcc ggc gaa caa ctc gac caa cca gca gga aca ctc 1008 Ser Phe Met Phe Ser Gly Glu Gln Leu Asp Gln Pro Ala Gly Thr Leu 325 330 335			
tcc ggc ggt gaa aaa acc cgc ctc gca ctg gcc acc ctc gtg tcc tcc 1056 Ser Gly Gly Glu Lys Thr Arg Leu Ala Leu Ala Thr Leu Val Ser Ser 340 345 350			
cgc gca aac gtc ctg ctt ctc gac gag ccc acc aac aac ctt gac ccg 1104 Arg Ala Asn Val Leu Leu Leu Asp Glu Pro Thr Asn Asn Leu Asp Pro 355 360 365			
atc tcc cgc gaa cag gtc ctc gac gca ctg cgc acc tac acc ggc gca 1152 Ile Ser Arg Glu Gln Val Leu Asp Ala Leu Arg Thr Tyr Thr Gly Ala 370 375 380			
gtc gtc ctg gtt acc cac gac ccg ggt gca aag gcc ctt gag cca 1200 Val Val Leu Val Thr His Asp Pro Gly Ala Val Lys Ala Leu Glu Pro 385 390 395 400			
gaa cgc gtc atc gtg ctt cct gat ggc acc gag gat ctt tgg aat gat 1248 Glu Arg Val Ile Val Leu Pro Asp Gly Thr Glu Asp Leu Trp Asn Asp 405 410 415			
cag tac atg gaa atc gtg gaa ttg gcg taggttctaa ggctgtttat 1295 Gln Tyr Met Glu Ile Val Glu Leu Ala 420 425			
gct 1298			
<210> 1104			
<211> 425			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 1104			
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Tyr Glu Ala Asp Ala Glu Ala Ala Gln Ile Cys Asp Asn Leu Gly Leu
20 25 30

Glu Ala Arg Ile Leu Asp Gln Gln Leu Lys Thr Leu Ser Gly Gly Gln
35 40 45

Arg Arg Arg Val Glu Leu Ala Gln Ile Leu Phe Ala Ala Thr Asn Gly
50 55 60

Ser Gly Lys Ser Lys Thr Thr Leu Leu Leu Asp Glu Pro Thr Asn His
65 70 75 80

Leu Asp Ala Asp Ser Ile Thr Trp Leu Arg Asp Phe Leu Ala Lys His
85 90 95

Glu Gly Gly Leu Ile Met Ile Ser His Asp Val Glu Leu Leu Gly Ala
100 105 110

Val Cys Asn Lys Ile Trp Tyr Leu Asp Ala Val Arg Ser Glu Ala Asp
115 120 125

Val Tyr Asn Met Gly Phe Ser Lys Tyr Val Asp Ala Arg Ala Leu Asp
130 135 140

Glu Ala Arg Arg Arg Glu Arg Ala Asn Ala Glu Lys Lys Ala Gly
145 150 155 160

Ala Leu Lys Asp Gln Ala Ala Arg Leu Gly Ala Lys Ala Thr Lys Ala
165 170 175

Ala Ala Ala Lys Gln Met Ile Ala Arg Ala Glu Arg Met Ile Asp Asn
180 185 190

Leu Asp Glu Ile Arg Val Ala Asp Arg Ala Ala Asn Ile Val Phe Pro
195 200 205

Glu Pro Ala Pro Cys Gly Lys Thr Pro Leu Asn Ala Lys Gly Leu Thr
210 215 220

Lys Met Tyr Gly Ser Leu Glu Val Phe Ala Gly Val Asp Leu Ala Ile
225 230 235 240

Asp Lys Gly Ser Arg Val Val Leu Gly Phe Asn Gly Ala Gly Lys
245 250 255

Thr Thr Leu Leu Lys Leu Leu Ala Gly Val Glu Arg Thr Asp Gly Glu
260 265 270

Gly Gly Ile Val Thr Gly Tyr Gly Leu Lys Ile Gly Tyr Phe Ala Gln
275 280 285

Glu His Asp Thr Ile Asp Pro Asp Lys Ser Val Trp Gln Asn Thr Ile
290 295 300

Glu Ala Cys Ala Asp Ala Asp Gln Gln Ser Leu Arg Ser Leu Leu Gly
305 310 315 320

Ser Phe Met Phe Ser Gly Glu Gln Leu Asp Gln Pro Ala Gly Thr Leu
325 330 335

Ser Gly Gly Glu Lys Thr Arg Leu Ala Leu Ala Thr Leu Val Ser Ser
 340 345 350
 Arg Ala Asn Val Leu Leu Leu Asp Glu Pro Thr Asn Asn Leu Asp Pro
 355 360 365
 Ile Ser Arg Glu Gln Val Leu Asp Ala Leu Arg Thr Tyr Thr Gly Ala
 370 375 380
 Val Val Leu Val Thr His Asp Pro Gly Ala Val Lys Ala Leu Glu Pro
 385 390 395 400
 Glu Arg Val Ile Val Leu Pro Asp Gly Thr Glu Asp Leu Trp Asn Asp
 405 410 415
 Gln Tyr Met Glu Ile Val Glu Leu Ala
 420 425

<210> 1105

<211> 613

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(613)

<223> RXN03171

<400> 1105

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 cggctttctt ctgggcggca atgatttaac atgtgaagct atg gac atc acc atc 115
 Met Asp Ile Thr Ile
 1 5

gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163
 Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu
 10 15 20

cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211
 Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Asn Asp Leu Gly Ala
 25 30 35

atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259
 Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp
 40 45 50

acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307
 Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro
 55 60 65

ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355
 Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro
 70 75 80 85

gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403
 Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala
 90 95 100

cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451

Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro			
105	110	115	
cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc			499
Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala			
120	125	130	
acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc			547
Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly			
135	140	145	
gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg			595
Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val			
150	155	160	165
gac gca ttg gcg gaa tct			613
Asp Ala Leu Ala Glu Ser			
170			
<210> 1106			
<211> 171			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 1106			
Met Asp Ile Thr Ile Val Asn His Pro Leu Val Ala Ser Arg Leu Thr			
1	5	10	15
Leu Leu Arg Asp Glu Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala			
20	25	30	
Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu			
35	40	45	
Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr			
50	55	60	
Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu			
65	70	75	80
Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly			
85	90	95	
Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr			
100	105	110	
Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val			
115	120	125	
Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu			
130	135	140	
Leu Ala Asp Arg Gly Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser			
145	150	155	160
Ala Gln Pro Gly Val Asp Ala Leu Ala Glu Ser			
165	170		

<210> 1107

<211> 613
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(613)
 <223> FRXA02857

<400> 1107
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 cggctttctt ctggcgca atgatttaac atgtgaagct atg gac atc acc atc 115
 Met Asp Ile Thr Ile
 1 5

gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163
 Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu
 . 10 15 20

cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211
 Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala
 25 30 35

atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259
 Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp
 40 45 50

acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307
 Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro
 55 60 65

ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355
 Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro
 70 75 80 85

gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403
 Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala
 90 95 100

cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451
 Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro
 105 110 115

cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499
 Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala
 120 125 130

acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc 547
 Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly
 135 140 145

gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595
 Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val
 150 155 160 165

gac gca ttg gcg gaa tct 613
 Asp Ala Leu Ala Glu Ser
 170

<210> 1108
<211> 171
<212> PRT
<213> Corynebacterium glutamicum

<400> 1108
Met Asp Ile Thr Ile Val Asn His Pro Leu Val Ala Ser Arg Leu Thr
1 5 10 15

Leu Leu Arg Asp Glu Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala
20 25 30

Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu
35 40 45

Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr
50 55 60

Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu
65 70 75 80

Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly
85 90 95

Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr
100 105 110

Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val
115 120 125

Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu
130 135 140

Leu Ala Asp Arg Gly Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser
145 150 155 160

Ala Gln Pro Gly Val Asp Ala Leu Ala Glu Ser
165 170

<210> 1109
<211> 424
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(424)
<223> RXN00450

<400> 1109
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gtttgataa tgatctggct cgggtggtgg gattcgacta gtg ggc gtt tta cct 115
Val Gly Val Leu Pro
1 5

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163
Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu
10 15 20

gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val 25	30	35	211
att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg 40	45	50	259
gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg 55	60	65	307
cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr 70	75	80	355
gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val 90	95	100	403
ggt gct cga atc gga cgc atc Gly Ala Arg Ile Gly Arg Ile 105			424

<210> 1110			
<211> 108			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 1110			
Val Gly Val Leu Pro Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg 1	5	10	15
Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val 20	25	30	
Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr 35	40	45	
Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu 50	55	60	
Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg 65	70	75	80
Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys 85	90	95	
Ala Gly Ala Leu Val Gly Ala Arg Ile Gly Arg Ile 100	105		

<210> 1111			
<211> 418			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)...(418)			

<223> FRXA00450

<400> 1111
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gtttgataa tgatctggct cgggtgggtgg gattcgacta gtg ggc gtt tta cct 115
Val Gly Val Leu Pro
1 5

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163
Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu
10 15 20

gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc 211
Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val
25 30 35

att tac gcg ccg acc ggg gag atc ctg cgc acc gca acg aac cgt cga 259
Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg
40 45 50

gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga 307
Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg
55 60 65

cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc 355
Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr
70 75 80 85

gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg 403
Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val
90 95 100

ggt gct cga atc gga 418
Gly Ala Arg Ile Gly
105

<210> 1112

<211> 106

<212> PRT

<213> Corynebacterium glutamicum

<400> 1112
Val Gly Val Leu Pro Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg
1 5 10 15

Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val
20 25 30

Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr
35 40 45

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu
50 55 60

Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg
65 70 75 80

Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys
85 90 95

Ala Gly Ala Leu Val Gly Ala Arg Ile Gly
100 105

<210> 1113

<211> 615

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(592)

<223> RXA00465

<400> 1113

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caagcgctac cagcgttgat gcgaggtttg agcgcctaac atg act gaa gat gac 115
Met Thr Glu Asp Asp
1 5tta gat ctg ctg cac cgc aca gta gaa cta gcc acc cag gca ctc aag 163
Leu Asp Leu Leu His Arg Thr Val Glu Leu Ala Thr Gln Ala Leu Lys
10 15 20cag gga aac agt cct tat gga tcc ctg ctg gtt gat ccc ttc ggc gcg 211
Gln Gly Asn Ser Pro Tyr Gly Ser Leu Leu Val Asp Pro Phe Gly Ala
25 30 35gtc gtt ttt gaa gac cac aac cga gat gcc gat ggg gat ctg acc aag 259
Val Val Phe Glu Asp His Asn Arg Asp Ala Asp Gly Asp Leu Thr Lys
40 45 50cac ccg gaa ttc gcc atc gcc aaa tat gcg atc gaa aat tac agt gca 307
His Pro Glu Phe Ala Ile Ala Lys Tyr Ala Ile Glu Asn Tyr Ser Ala
55 60 65tca gaa cgt gct gcg tgc act gtt tat acc tcg acg gaa cat tgc gcg 355
Ser Glu Arg Ala Ala Cys Thr Val Tyr Thr Ser Thr Glu His Cys Ala
70 75 80 85atg tgc gcc ggt gcc cat gcg tgg gct gga ctg ggc aaa att tac tgc 403
Met Cys Ala Gly Ala His Ala Trp Ala Gly Leu Gly Lys Ile Tyr Cys
90 95 100gcc acc aca ggt ggg caa aca gcc gct tgg tac gca aag tgg ggt gca 451
Ala Thr Thr Gly Gly Gln Thr Ala Ala Trp Tyr Ala Lys Trp Gly Ala
105 110 115gaa tct ggg cct ttg aac ccg att tca gcg gac aaa att agc ccg aac 499
Glu Ser Gly Pro Leu Asn Pro Ile Ser Ala Asp Lys Ile Ser Pro Asn
120 125 130ata tcc atc gaa gga cct gct tcc aga ttt gag gaa gtc ctg tat gaa 547
Ile Ser Ile Glu Gly Pro Ala Ser Arg Phe Glu Glu Val Leu Tyr Glu
135 140 145ctg cat cga tgg ttt tat tta ggg cag tct ccg aat aag gct ctt 592
Leu His Arg Trp Phe Tyr Leu Gly Gln Ser Pro Asn Lys Ala Leu
150 155 160

tagcgctggg catgtgactt taa

615

<210> 1114

<211> 164

<212> PRT

<213> Corynebacterium glutamicum

<400> 1114

Met	Thr	Glu	Asp	Asp	Leu	Asp	Leu	Leu	His	Arg	Thr	Val	Glu	Leu	Ala
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Thr	Gln	Ala	Leu	Lys	Gln	Gly	Asn	Ser	Pro	Tyr	Gly	Ser	Leu	Leu	Val
							20	25					30		

Asp	Pro	Phe	Gly	Ala	Val	Val	Phe	Glu	Asp	His	Asn	Arg	Asp	Ala	Asp
							35	40				45			

Gly	Asp	Leu	Thr	Lys	His	Pro	Glu	Phe	Ala	Ile	Ala	Lys	Tyr	Ala	Ile
							50	55				60			

Glu	Asn	Tyr	Ser	Ala	Ser	Glu	Arg	Ala	Ala	Cys	Thr	Val	Tyr	Thr	Ser
						65		70		75			80		

Thr	Glu	His	Cys	Ala	Met	Cys	Ala	Gly	Ala	His	Ala	Trp	Ala	Gly	Leu
							85		90			95			

Gly	Lys	Ile	Tyr	Cys	Ala	Thr	Thr	Gly	Gly	Gln	Thr	Ala	Ala	Trp	Tyr
						100		105				110			

Ala	Lys	Trp	Gly	Ala	Glu	Ser	Gly	Pro	Leu	Asn	Pro	Ile	Ser	Ala	Asp
							115	120				125			

Lys	Ile	Ser	Pro	Asn	Ile	Ser	Ile	Glu	Gly	Pro	Ala	Ser	Arg	Phe	Glu
							130	135				140			

Glu	Val	Leu	Tyr	Glu	Leu	His	Arg	Trp	Phe	Tyr	Leu	Gly	Gln	Ser	Pro
						145		150		155			160		

Asn Lys Ala Leu

<210> 1115

<211> 1083

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1060)

<223> RXA00717

<400> 1115

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tcaatttcat	acgtttctc	tcaagattaa	ggacacttac	gtg	acc	cca	ccc	gct	115
				Val	Thr	Pro	Pro	Ala	
					1			5	

cgc cga gat ggc aca ccg gac aag aag cag agc aat cgc tct ggc gga	163
Arg Arg Asp Gly Thr Pro Asp Lys Lys Gln Ser Asn Arg Ser Gly Gly	
10	15
15	20
tac cgg tct tca gtt cgt ggc tac aag cca gga tca tcc cgc cca aac	211
Tyr Arg Ser Ser Val Arg Gly Tyr Lys Pro Gly Ser Ser Arg Pro Asn	
25	30
30	35
aca cgc cag cag cct cag aag aag gat gag att ctt ctc tcc aac gct	259
Thr Arg Gln Gln Pro Gln Lys Lys Asp Glu Ile Leu Leu Ser Asn Ala	
40	45
45	50
aag cct gcc aag aag caa aac gta aaa tcc gac gac gat tgg tcg atg	307
Lys Pro Ala Lys Lys Gln Asn Val Lys Ser Asp Asp Asp Trp Ser Met	
55	60
60	65
ggg ttc tta aac cgc aat gac tct gac gga gtt cgc ctg cag aag gtg	355
Gly Phe Leu Asn Arg Asn Asp Ser Asp Gly Val Arg Leu Gln Lys Val	
70	75
75	80
80	85
ctt gcc caa gca ggt gtg gca tca cgt cga cac gca gaa atc ctg att	403
Leu Ala Gln Ala Gly Val Ala Ser Arg Arg His Ala Glu Ile Leu Ile	
90	95
95	100
gat cag ggc cgt gtg gag gtc aac gat cgt atc gtg acc acc cag ggc	451
Asp Gln Gly Arg Val Glu Val Asn Asp Arg Ile Val Thr Thr Gln Gly	
105	110
110	115
gtg cgc gtg gat cca aac aac gat gtc atc cgt gtt gac ggc gtc cgc	499
Val Arg Val Asp Pro Asn Asn Asp Val Ile Arg Val Asp Gly Val Arg	
120	125
125	130
atc cac atc aac gag gac ctc gag tac ttc gtg ctc aac aag cct cgt	547
Ile His Ile Asn Glu Asp Leu Glu Tyr Phe Val Leu Asn Lys Pro Arg	
135	140
140	145
ggc atg cac tcc acc atg agc gat gaa ctt ggt cgc cca tgc gtg ggt	595
Gly Met His Ser Thr Met Ser Asp Glu Leu Gly Arg Pro Cys Val Gly	
150	155
155	160
160	165
gat ctg gtc agt gag aag act gca tct gga cag cgt ctg ttc cac gtc	643
Asp Leu Val Ser Glu Lys Thr Ala Ser Gly Gln Arg Leu Phe His Val	
170	175
175	180
180	
ggt cgc ctc gac gcg gac acc gaa ggt ttg ctg ctg ctc acc aac gat	691
Gly Arg Leu Asp Ala Asp Thr Glu Gly Leu Leu Leu Thr Asn Asp	
185	190
190	195
195	
ggt gag ttg gct aac cgc ctc atg cac cct aag tac gaa gtg tcc aag	739
Gly Glu Leu Ala Asn Arg Leu Met His Pro Lys Tyr Glu Val Ser Lys	
200	205
205	210
210	
act tac ctt gct acc gtt cgc ggt gaa gca acc aat aag cta gtc agc	787
Thr Tyr Leu Ala Thr Val Arg Gly Glu Ala Thr Asn Lys Leu Val Ser	
215	220
220	225
225	
gct ctt cgt gat ggc gtg gag ttg gaa gat ggc cct gcc aag gct gac	835
Ala Leu Arg Asp Gly Val Glu Leu Glu Asp Gly Pro Ala Lys Ala Asp	
230	235
235	240
240	245
245	
ttt gcg cag att atc gac gta ttc cag ggc aag tcc ttg ttg cgc atc	883

Phe Ala Gln Ile Ile Asp Val Phe Gln Gly Lys Ser Leu Leu Arg Ile			
250	255	260	
gaa atc cac gaa ggc cgc aag cac att gtg cga cgc ctc ttc gat gag		931	
Glu Ile His Glu Gly Arg Lys His Ile Val Arg Arg Leu Phe Asp Glu			
265	270	275	
ctc ggt ttc cca gtc gag cgc ctc gtg cgc acc aag ctg cac acc gtt		979	
Leu Gly Phe Pro Val Glu Arg Leu Val Arg Thr Lys Leu His Thr Val			
280	285	290	
cag ctt ggt gat cag aag cca ggt tcc ctt cgt gca ctg aac tcc tct			
1027			
Gln Leu Gly Asp Gln Lys Pro Gly Ser Leu Arg Ala Leu Asn Ser Ser			
295	300	305	
gag ctg acc agc tta tac aag gtg gtc caa ctg tgacggaaat ttccaacatg			
1080			
Glu Leu Thr Ser Leu Tyr Lys Val Val Gln Leu			
310	315	320	
cct			
1083			
<210> 1116			
<211> 320			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 1116			
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Asn Arg Ser Gly Gly Tyr Arg Ser Ser Val Arg Gly Tyr Lys Pro Gly			
20	25	30	
Ser Ser Arg Pro Asn Thr Arg Gln Gln Pro Gln Lys Lys Asp Glu Ile			
35	40	45	
Leu Leu Ser Asn Ala Lys Pro Ala Lys Lys Gln Asn Val Lys Ser Asp			
50	55	60	
Asp Asp Trp Ser Met Gly Phe Leu Asn Arg Asn Asp Ser Asp Gly Val			
65	70	75	80
Arg Leu Gln Lys Val Leu Ala Gln Ala Gly Val Ala Ser Arg Arg His			
85	90	95	
Ala Glu Ile Leu Ile Asp Gln Gly Arg Val Glu Val Asn Asp Arg Ile			
100	105	110	
Val Thr Thr Gln Gly Val Arg Val Asp Pro Asn Asn Asp Val Ile Arg			
115	120	125	
Val Asp Gly Val Arg Ile His Ile Asn Glu Asp Leu Glu Tyr Phe Val			
130	135	140	
Leu Asn Lys Pro Arg Gly Met His Ser Thr Met Ser Asp Glu Leu Gly			
145	150	155	160

Arg Pro Cys Val Gly Asp Leu Val Ser Glu Lys Thr Ala Ser Gly Gln
165 170 175

Arg Leu Phe His Val Gly Arg Leu Asp Ala Asp Thr Glu Gly Leu Leu
180 185 190

Leu Leu Thr Asn Asp Gly Glu Leu Ala Asn Arg Leu Met His Pro Lys
195 200 205

Tyr Glu Val Ser Lys Thr Tyr Leu Ala Thr Val Arg Gly Glu Ala Thr
210 215 220

Asn Lys Leu Val Ser Ala Leu Arg Asp Gly Val Glu Leu Glu Asp Gly
225 230 235 240

Pro Ala Lys Ala Asp Phe Ala Gln Ile Ile Asp Val Phe Gln Gly Lys
245 250 255

Ser Leu Leu Arg Ile Glu Ile His Glu Gly Arg Lys His Ile Val Arg
260 265 270

Arg Leu Phe Asp Glu Leu Gly Phe Pro Val Glu Arg Leu Val Arg Thr
275 280 285

Lys Leu His Thr Val Gln Leu Gly Asp Gln Lys Pro Gly Ser Leu Arg
290 295 300

Ala Leu Asn Ser Ser Glu Leu Thr Ser Leu Tyr Lys Val Val Gln Leu
305 310 315 320

<210> 1117

<211> 978

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(955)

<223> RXA01894

<400> 1117

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acccatgaat gaaccggagc aacatcaccg gtccatgagg atg ccc aaa ccc aaa 115
Met Pro Lys Pro Lys
1 5

aat aat gcg ggt cga gat ctc aaa gct gcc att gct gtg ggg atc gga 163
Asn Asn Ala Gly Arg Asp Leu Lys Ala Ala Ile Ala Val Gly Ile Gly
10 15 20

ctg ggg gtc ctg gtt ctt ttg ggg att gtc cta agc cca tgg ggt tgg 211
Leu Gly Val Leu Val Leu Leu Gly Ile Val Leu Ser Pro Trp Gly Trp
25 30 35

tac atc ctc gtt gca ggt ttt atg gct gca gca aca tgg gaa gtt ggt 259
Tyr Ile Leu Val Ala Gly Phe Met Ala Ala Thr Trp Glu Val Gly

40	45	50	
agc aga ctt aaa gaa ggc ggc tat cat ttg cca ctg ccg att atg atc Ser Arg Leu Lys Glu Gly Gly Tyr His Leu Pro Leu Pro Ile Met Ile	55	60	307
		65	
atc ggc ggt cag gca atc atc tgg ctg tca tgg cca ttt ggc acg atg Ile Gly Gly Gln Ala Ile Ile Trp Leu Ser Trp Pro Phe Gly Thr Met	70	75	355
		80	85
ggc att ttg gcg tct ttt gtg gcc act gtg ttg gtg ctg atg tat ttc Gly Ile Leu Ala Ser Phe Val Ala Thr Val Leu Val Leu Met Tyr Phe	90	95	403
		100	
cga att ttc tac aat ggc acg gaa aaa gaa gcc cgcc aac tat ttg agg Arg Ile Phe Tyr Asn Gly Thr Glu Lys Glu Ala Arg Asn Tyr Leu Arg	105	110	451
		115	
gac acc tct gtg ggc atc ttc gtg ctc acc tgg att cca ttg ttc gga Asp Thr Ser Val Gly Ile Phe Val Leu Thr Trp Ile Pro Leu Phe Gly	120	125	499
		130	
agc ttc gct gcg atg ctg tcg ctg atg caa aac aat tcc atc ccg ggt Ser Phe Ala Ala Met Leu Ser Leu Met Gln Asn Asn Ser Ile Pro Gly	135	140	547
		145	
aca tat ttc att ttg acg ttc atg ctg tgt gtg atc gca tcg gat gtg Thr Tyr Phe Ile Leu Thr Phe Met Leu Cys Val Ile Ala Ser Asp Val	150	155	595
		160	165
ggc ggg tat atc gcg ggt gtg ttc ttt gga tcg cac cca atg gcg ccg Gly Gly Tyr Ile Ala Gly Val Phe Phe Gly Ser His Pro Met Ala Pro	170	175	643
		180	
ttg gtg agt ccg aag aag tct tgg gaa ggc ttt gcc ggc tcc att gtc Leu Val Ser Pro Lys Lys Ser Trp Glu Gly Phe Ala Gly Ser Ile Val	185	190	691
		195	
tta gga tcg gtc act ggt gca ctc agt gtt cac ttc ctg ctc gat cac Leu Gly Ser Val Thr Gly Ala Leu Ser Val His Phe Leu Leu Asp His	200	205	739
		210	
cac tgg tgg atg ggt gtg atc ttg ggt tgt gcc cta gtt gtg tgc gcc His Trp Trp Met Gly Val Ile Leu Gly Cys Ala Leu Val Val Cys Ala	215	220	787
		225	
acg ttg ggt gac ttg gtt gag tcg cag ttc aaa cgc gat ttg ggc atc Thr Leu Gly Asp Leu Val Glu Ser Gln Phe Lys Arg Asp Leu Gly Ile	230	235	835
		240	245
aag gat atg tcg aac ctt ctt cca ggc cac ggc gga ttg atg gac cgt Lys Asp Met Ser Asn Leu Leu Pro Gly His Gly Gly Leu Met Asp Arg	250	255	883
		260	
ttg gat ggc atg ctc ccg gcc gcg atg gtg acg tgg ttg atc ctg agt Leu Asp Gly Met Leu Pro Ala Ala Met Val Thr Trp Leu Ile Leu Ser	265	270	931
		275	
gtg atc agc agc tcg tat ccg tcg taaaagcttgg gccagcttta agt Val Ile Ser Ser Ser Tyr Pro Ser	280	285	978

<210> 1118

<211> 285

<212> PRT

<213> Corynebacterium glutamicum

<400> 1118

Met Pro Lys Pro Lys Asn Asn Ala Gly Arg Asp Leu Lys Ala Ala Ile
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Ala Val Gly Ile Gly Leu Gly Val Leu Val Leu Leu Gly Ile Val Leu
20 25 30

Ser Pro Trp Gly Trp Tyr Ile Leu Val Ala Gly Phe Met Ala Ala Ala
35 40 45

Thr Trp Glu Val Gly Ser Arg Leu Lys Glu Gly Gly Tyr His Leu Pro
50 55 60

Leu Pro Ile Met Ile Ile Gly Gly Gln Ala Ile Ile Trp Leu Ser Trp
65 70 75 80

Pro Phe Gly Thr Met Gly Ile Leu Ala Ser Phe Val Ala Thr Val Leu
85 90 95

Val Leu Met Tyr Phe Arg Ile Phe Tyr Asn Gly Thr Glu Lys Glu Ala
100 105 110

Arg Asn Tyr Leu Arg Asp Thr Ser Val Gly Ile Phe Val Leu Thr Trp
115 120 125

Ile Pro Leu Phe Gly Ser Phe Ala Ala Met Leu Ser Leu Met Gln Asn
130 135 140

Asn Ser Ile Pro Gly Thr Tyr Phe Ile Leu Thr Phe Met Leu Cys Val
145 150 155 160

Ile Ala Ser Asp Val Gly Gly Tyr Ile Ala Gly Val Phe Phe Gly Ser
165 170 175

His Pro Met Ala Pro Leu Val Ser Pro Lys Lys Ser Trp Glu Gly Phe
180 185 190

Ala Gly Ser Ile Val Leu Gly Ser Val Thr Gly Ala Leu Ser Val His
195 200 205

Phe Leu Leu Asp His His Trp Trp Met Gly Val Ile Leu Gly Cys Ala
210 215 220

Leu Val Val Cys Ala Thr Leu Gly Asp Leu Val Glu Ser Gln Phe Lys
225 230 235 240

Arg Asp Leu Gly Ile Lys Asp Met Ser Asn Leu Leu Pro Gly His Gly
245 250 255

Gly Leu Met Asp Arg Leu Asp Gly Met Leu Pro Ala Ala Met Val Thr
260 265 270

Trp Leu Ile Leu Ser Val Ile Ser Ser Ser Tyr Pro Ser
275 280 285

<210> 1119
 <211> 879
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(856)
 <223> RXA02536

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 Met Asp Asn Phe Ala
 1 5

ctg ctg cgt gat gct gaa aaa gct gcg gaa cag ggg gct cggt 163
 Leu Leu Arg Asp Ala Ala Glu Lys Ala Ala Glu Gln Gly Ala Arg Val
 10 15 20

ttg gtg ttt ccg gag gcg act tcg caa agc ttt ggt acg gga agg ctt 211
 Leu Val Phe Pro Glu Ala Thr Ser Gln Ser Phe Gly Thr Gly Arg Leu
 25 30 35

gat act cag gcg gag gag ctc gat ggc gaa ttc tcc acc gcg gta cga 259
 Asp Thr Gln Ala Glu Glu Leu Asp Gly Glu Phe Ser Thr Ala Val Arg
 40 45 50

aaa tta gcc gat gag ctg gac gtt gtc atc gtt gcg ggc atg ttc acc 307
 Lys Leu Ala Asp Glu Leu Asp Val Val Ile Val Ala Gly Met Phe Thr
 55 60 65

cct gct gac acc gtg cag cgc ggt gaa aaa acg atc tcg cgc gtc aac 355
 Pro Ala Asp Thr Val Gln Arg Gly Glu Lys Thr Ile Ser Arg Val Asn
 70 75 80 85

aac acc gtg ctg att agt ggc gct gga ttg cat cag gga tac aac aaa 403
 Asn Thr Val Leu Ile Ser Gly Ala Gly Leu His Gln Gly Tyr Asn Lys
 90 95 100

att cac aca tat gac gcg ttc ggt tat agg gaa tcc gac act gtg aaa 451
 Ile His Thr Tyr Asp Ala Phe Gly Tyr Arg Glu Ser Asp Thr Val Lys
 105 110 115

ccg ggc gat gag ctg gtt gta ttc gag gtc gac gat att aaa ttt ggt 499
 Pro Gly Asp Glu Leu Val Val Phe Glu Val Asp Asp Ile Lys Phe Gly
 120 125 130

gtg gcg aca tgc tac gat att cga ttc cca gaa cag ttc aaa gac ctc 547
 Val Ala Thr Cys Tyr Asp Ile Arg Phe Pro Glu Gln Phe Lys Asp Leu
 135 140 145

gcc cgc aac ggt gca cag ata att gtg gtt ccc acg tcg tgg caa gac 595
 Ala Arg Asn Gly Ala Gln Ile Ile Val Val Pro Thr Ser Trp Gln Asp
 150 155 160 165

ggt cct gga aaa tta gaa caa tgg gaa gtc ctc cct cgc gcg cgt gca 643
 Gly Pro Gly Lys Leu Glu Gln Trp Glu Val Leu Pro Arg Ala Arg Ala

170	175	180	
ctg gat tcc acc tgc tgg atc gta gcg tgt ggg caa gcg cga ctt cca Leu Asp Ser Thr Cys Trp Ile Val Ala Cys Gly Gln Ala Arg Leu Pro 185	190	195	691
gaa gaa tta cgc gat gaa cga aaa ggc cct acg ggg att ggt cat tcc Glu Glu Leu Arg Asp Glu Arg Lys Gly Pro Thr Gly Ile Gly His Ser 200	205	210	739
atg gtg aca aac cca cac ggt gaa gta att gct agc gcg ggt tat gag Met Val Thr Asn Pro His Gly Glu Val Ile Ala Ser Ala Gly Tyr Glu 215	220	225	787
cca gaa atg ttg atc gcg gat att gat gtc agc ggt ttg gcc aaa att Pro Glu Met Leu Ile Ala Asp Ile Asp Val Ser Gly Leu Ala Lys Ile 230	235	240	835
cg ^g gag gca ttg cct gtt ctt taaccactgt ctaaggaatc act Arg Glu Ala Leu Pro Val Leu 250			879
<210> 1120			
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Gln Gly Ala Arg Val Leu Val Phe Pro Glu Ala Thr Ser Gln Ser Phe 20 25 30			
Gly Thr Gly Arg Leu Asp Thr Gln Ala Glu Glu Leu Asp Gly Glu Phe 35 40 45			
Ser Thr Ala Val Arg Lys Leu Ala Asp Glu Leu Asp Val Val Ile Val 50 55 60			
Ala Gly Met Phe Thr Pro Ala Asp Thr Val Gln Arg Gly Glu Lys Thr 65 70 75 80			
Ile Ser Arg Val Asn Asn Thr Val Leu Ile Ser Gly Ala Gly Leu His 85 90 95			
Gln Gly Tyr Asn Lys Ile His Thr Tyr Asp Ala Phe Gly Tyr Arg Glu 100 105 110			
Ser Asp Thr Val Lys Pro Gly Asp Glu Leu Val Val Phe Glu Val Asp 115 120 125			
Asp Ile Lys Phe Gly Val Ala Thr Cys Tyr Asp Ile Arg Phe Pro Glu 130 135 140			
Gln Phe Lys Asp Leu Ala Arg Asn Gly Ala Gln Ile Ile Val Val Pro 145 150 155 160			
Thr Ser Trp Gln Asp Gly Pro Gly Lys Leu Glu Gln Trp Glu Val Leu 165 170 175			

Pro Arg Ala Arg Ala Leu Asp Ser Thr Cys Trp Ile Val Ala Cys Gly
 180 185 190

Gln Ala Arg Leu Pro Glu Glu Leu Arg Asp Glu Arg Lys Gly Pro Thr
 195 200 205

Gly Ile Gly His Ser Met Val Thr Asn Pro His Gly Glu Val Ile Ala
 210 215 220

Ser Ala Gly Tyr Glu Pro Glu Met Leu Ile Ala Asp Ile Asp Val Ser
 225 230 235 240

Gly Leu Ala Lys Ile Arg Glu Ala Leu Pro Val Leu
 245 250

<210> 1121

<211> 1528

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1528)

<223> RXN01209

<400> 1121

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ctttatgacg tggatgccc ggctgtggcc tcgttggttg atg tgc gag agg cct 115
 Met Cys Glu Arg Pro
 1 5

gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163
 Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val
 10 15 20

ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att 211
 Leu Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile
 25 30 35

tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg 259
 Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val
 40 45 50

gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct 307
 Glu Asp Val Arg Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala
 55 60 65

cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag 355
 Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu
 70 75 80 85

ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa 403
 Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln
 90 95 100

gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa 451
 Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu
 105 110 115

aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly 120	125	130	499	
gtg gca ttg ccc gat gtg att ggc att ggt ccg gtg gcc tct act gcg Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala 135	140	145	547	
acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag ggc atc gct gag Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu 150	155	160	165	595
atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly 170	175	180	643	
ggc gtt ggt cta cgc aac gcg gcc gaa ctc gct gct acg ccc atc gac Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Ala Thr Pro Ile Asp 185	190	195	691	
ggt ctg tgc gtg gtc tct gaa atc atg acc gcc gcc aat cca gca gct Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala 200	205	210	739	
gcg gca act cgc ctg cgg act gct ttt caa cct act ttc tcg cct gaa Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu 215	220	225	787	
act caa act gaa ctc tct caa aca gaa ctc caa gga gcc ttc gtg aat Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn 230	235	240	245	835
tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr 250	255	260	883	
ggt ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly 265	270	275	931	
ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His 280	285	290	979	
ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag 1027				
Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln 295	300	305		
ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc 1075				
Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly 310	315	320	325	
atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt 1123				
Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly 330	335	340		

tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc
1171
Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr
345 350 355

agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc
1219
Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg
360 365 370

ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc
1267
Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala
375 380 385

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct
1315
Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala
390 395 400 405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag
1363
Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys
410 415 420

ggt gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc
1411
Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro
425 430 435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac
1459
Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn
440 445 450

tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc
1507
Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile
455 460 465

gcc gcc ggc gaa agc gtg gaa
1528
Ala Ala Gly Glu Ser Val Glu
470 475

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Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp
35 40 45

Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys
50 55 60

Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu
65 70 75 80

Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp
85 90 95

Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu
100 105 110

Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln
115 120 125

Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro
130 135 140

Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val
145 150 155 160

Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala
165 170 175

Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala
180 185 190

Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala
195 200 205

Ala Asn Pro Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro
210 215 220

Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln
225 230 235 240

Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala
245 250 255

Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser
260 265 270

Ile Ala Ala Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val
275 280 285

Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr
290 295 300

Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp
305 310 315 320

Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val
325 330 335

Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro
340 345 350

Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu
355 360 365

Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn

370	375	380	
Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met			
385	390	395	400
Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr			
405	410	415	
Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn			
420	425	430	
Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg			
435	440	445	
Val Asn Thr Thr Asn Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser			
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Leu Ala Thr Lys Ile Ala Ala Gly Glu Ser Val Glu			
465	470	475	

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<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1528)
<223> FRXA01209

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Met Cys Glu Arg Pro
1 5

gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163
Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val
10 15 20

ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att 211
Leu Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile
25 30 35

tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg 259
Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val
40 45 50

gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct 307
Glu Asp Val Arg Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala
55 60 65

cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag 355
Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu
70 75 80 85

ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa 403
Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln
90 95 100

gca	cgg	gag	ctg	ctt	cca	gct	cat	ctt	gaa	ttg	ggt	ttg	agc	att	gaa	451
Ala	Arg	Glu	Leu	Leu	Pro	Ala	His	Leu	Glu	Leu	Gly	Leu	Ser	Ile	Glu	
105								110					115			
aac	ctg	gat	caa	ttg	cat	gct	gtg	atc	gcg	cag	tgc	gcc	gag	act	ggt	499
Asn	Leu	Asp	Gln	Leu	His	Ala	Val	Ile	Ala	Gln	Cys	Ala	Glu	Thr	Gly	
120							125					130				
gtg	gca	ttg	ccc	gat	gtg	att	ggc	att	ggt	ccg	gtg	gcc	tct	act	gcg	547
Val	Ala	Leu	Pro	Asp	Val	Ile	Gly	Ile	Gly	Pro	Val	Ala	Ser	Thr	Ala	
135							140					145				
acc	aaa	cca	gat	gcg	gca	ccc	gca	ttg	ggt	gtg	gag	ggc	atc	gct	gag	595
Thr	Lys	Pro	Asp	Ala	Ala	Pro	Ala	Leu	Gly	Val	Glu	Gly	Ile	Ala	Glu	
150							155				160		165			
atc	gcc	gct	gta	gct	caa	gac	cac	ggc	atc	gca	tca	gta	gct	att	gga	643
Ile	Ala	Ala	Val	Ala	Gln	Asp	His	Gly	Ile	Ala	Ser	Val	Ala	Ile	Gly	
170							175					180				
ggc	gtt	ggt	cta	cgc	aac	gcg	gcc	gaa	ctc	gct	gct	acg	ccc	atc	gac	691
Gly	Val	Gly	Leu	Arg	Asn	Ala	Ala	Glu	Leu	Ala	Ala	Thr	Pro	Ile	Asp	
185							190					195				
ggt	ctg	tgc	gtg	gtc	tct	gaa	atc	atg	acc	gcc	gcc	aat	cca	gca	gct	739
Gly	Leu	Cys	Val	Val	Ser	Glu	Ile	Met	Thr	Ala	Ala	Asn	Pro	Ala	Ala	
200							205					210				
gcg	gca	act	cgc	ctg	cg	act	gct	ttt	caa	cct	act	ttc	tcg	cct	gaa	787
Ala	Ala	Thr	Arg	Leu	Arg	Thr	Ala	Phe	Gln	Pro	Thr	Phe	Ser	Pro	Glu	
215							220					225				
act	caa	act	gaa	ctc	tct	caa	aca	gaa	ctc	caa	gga	gcc	ttc	tg	aat	835
Thr	Gln	Thr	Glu	Leu	Ser	Gln	Thr	Glu	Leu	Gln	Gly	Ala	Phe	Val	Asn	
230							235					240		245		
tcg	cct	tct	gcc	cca	cgt	gtg	ttg	tct	att	gca	ggc	act	gat	ccc	aca	883
Ser	Pro	Ser	Ala	Pro	Arg	Val	Leu	Ser	Ile	Ala	Gly	Thr	Asp	Pro	Thr	
250							255					260				
ggt	ggt	gca	ggt	att	cag	gct	gat	ctg	aag	tcc	att	gca	gca	ggt	ggc	931
Gly	Gly	Ala	Gly	Ile	Gln	Ala	Asp	Leu	Lys	Ser	Ile	Ala	Ala	Gly	Gly	
265							270					275				
ggc	tac	ggc	atg	tgc	gtt	gtg	acc	tcg	ctg	gtc	gcg	caa	aac	acc	cac	979
Gly	Tyr	Gly	Met	Cys	Val	Val	Thr	Ser	Leu	Val	Ala	Gln	Asn	Thr	His	
280							285					290				
ggc	gtc	aac	acg	atc	cac	acc	cca	ccc	ttg	acc	ttt	ttg	gaa	gaa	cag	1027
Gly	Val	Asn	Thr	Ile	His	Thr	Pro	Pro	Leu	Thr	Phe	Leu	Glu	Glu	Gln	
295							300					305				
ctg	gaa	gcg	gtc	ttt	tcc	gat	gtc	acc	gtc	gat	gcc	atc	aag	ctc	ggc	1075
Leu	Glu	Ala	Val	Phe	Ser	Asp	Val	Thr	Val	Asp	Ala	Ile	Lys	Leu	Gly	
310							315					320		325		
atg	ttg	ggc	tct	gcc	gac	acc	gtc	gat	ctg	gtg	gct	tca	tgg	ctt	gg	1123

Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly
330 335 340

tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc
1171

Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr
345 350 355

agc ggt gat cgc cta ctg gat gcg agc gct gaa tcg ctg cgc cgc
1219

Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg
360 365 370

ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc
1267

Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala
375 380 385

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct
1315

Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala
390 395 400 405

cag gct cag gga ttt gcg cg act cat gac acc atc gtc att gtc aag
1363

Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys
410 415 420

ggt gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc
1411

Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro
425 430 435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac
1459

Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn
440 445 450

tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc
1507

Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile
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1528

Ala Ala Gly Glu Ser Val Glu
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<211> 476

<212> PRT

<213> Corynebacterium glutamicum

<400> 1124

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Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp
35 40 45

Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys
50 55 60

Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu
65 70 75 80

Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp
85 90 95

Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu
100 105 110

Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln
115 120 125

Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro
130 135 140

Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val
145 150 155 160

Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala
165 170 175

Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala
180 185 190

Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala
195 200 205

Ala Asn Pro Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro
210 215 220

Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln
225 230 235 240

Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala
245 250 255

Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser
260 265 270

Ile Ala Ala Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val
275 280 285

Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr
290 295 300

Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp
305 310 315 320

Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val
325 330 335

Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro
340 345 350

Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu

355

360

365

Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn
 370 375 380

Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met
 385 390 395 400

Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr
 405 410 415

Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn
 420 425 430

Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg
 435 440 445

Val Asn Thr Thr Asn Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser
 450 455 460

Leu Ala Thr Lys Ile Ala Ala Gly Glu Ser Val Glu
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<211> 795

<212> DNA

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<220>

<221> CDS

<222> (101)..(772)

<223> RXN01617

<400> 1125

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 Leu Ile Leu Lys Thr
 1 5

act gga atc acc gtt ttg tcc cgg ttt gat gcg cag gtt atc gct aat 163
 Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala Gln Val Ile Ala Asn
 10 15 20

cag att gag gcc gcc acc gca gcg cac gat ctt gat gtg gtg aag atc 211
 Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val Lys Ile
 25 30 35

ggt atg ttg ggt act cct gca acg atc gat act gtg gca acc gct ttg 259
 Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr Ala Leu
 40 45 50

gag gaa aac agc ttc aag cac gtt gtc cta gac ccg gta ctg atc tgc 307
 Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu Ile Cys
 55 60 65

aag ggc cag gag ccc ggc gcg gca ctt gat act gac act gcc ctt cgc 355
 Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala Leu Arg
 70 75 80 85

gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac ttc gag	403																																																																				
Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn Phe Glu																																																																					
90	95		100	gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac gac ctg	451	Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp Asp Leu		105	110		115	aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac gtc gtt	499	Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr Val Val		120	125		130	gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac gta ctt	547	Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp Val Leu		135	140		145	ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc ggc gac	595	Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile Gly Asp		150	155		160		165	gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc acc gca	643	Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile Thr Ala		170	175		180	gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc gct aag	691	Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr Ala Lys		185	190		195	cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac gca ccg	739	Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn Ala Pro		200	205		210	ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt aaacaagctc	792	Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys		215	220	cct	795
	100																																																																				
gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac gac ctg	451																																																																				
Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp Asp Leu																																																																					
105	110		115	aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac gtc gtt	499	Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr Val Val		120	125		130	gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac gta ctt	547	Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp Val Leu		135	140		145	ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc ggc gac	595	Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile Gly Asp		150	155		160		165	gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc acc gca	643	Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile Thr Ala		170	175		180	gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc gct aag	691	Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr Ala Lys		185	190		195	cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac gca ccg	739	Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn Ala Pro		200	205		210	ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt aaacaagctc	792	Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys		215	220	cct	795								
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Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr Val Val																																																																					
120	125		130	gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac gta ctt	547	Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp Val Leu		135	140		145	ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc ggc gac	595	Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile Gly Asp		150	155		160		165	gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc acc gca	643	Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile Thr Ala		170	175		180	gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc gct aag	691	Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr Ala Lys		185	190		195	cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac gca ccg	739	Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn Ala Pro		200	205		210	ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt aaacaagctc	792	Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys		215	220	cct	795																
	130																																																																				
gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac gta ctt	547																																																																				
Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp Val Leu																																																																					
135	140		145	ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc ggc gac	595	Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile Gly Asp		150	155		160		165	gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc acc gca	643	Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile Thr Ala		170	175		180	gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc gct aag	691	Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr Ala Lys		185	190		195	cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac gca ccg	739	Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn Ala Pro		200	205		210	ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt aaacaagctc	792	Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys		215	220	cct	795																								
	145																																																																				
ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc ggc gac	595																																																																				
Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile Gly Asp																																																																					
150	155		160		165	gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc acc gca	643	Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile Thr Ala		170	175		180	gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc gct aag	691	Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr Ala Lys		185	190		195	cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac gca ccg	739	Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn Ala Pro		200	205		210	ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt aaacaagctc	792	Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys		215	220	cct	795																																
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	165																																																																				
gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc acc gca	643																																																																				
Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile Thr Ala																																																																					
170	175		180	gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc gct aag	691	Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr Ala Lys		185	190		195	cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac gca ccg	739	Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn Ala Pro		200	205		210	ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt aaacaagctc	792	Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys		215	220	cct	795																																										
	180																																																																				
gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc gct aag	691																																																																				
Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr Ala Lys																																																																					
185	190		195	cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac gca ccg	739	Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn Ala Pro		200	205		210	ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt aaacaagctc	792	Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys		215	220	cct	795																																																		
	195																																																																				
cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac gca ccg	739																																																																				
Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn Ala Pro																																																																					
200	205		210	ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt aaacaagctc	792	Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys		215	220	cct	795																																																										
	210																																																																				
ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt aaacaagctc	792																																																																				
Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys																																																																					
215	220																																																																				
cct	795																																																																				

<210> 1126

<211> 224

<212> PRT

<213> Corynebacterium glutamicum

<400> 1126

Leu Ile Leu Lys Thr Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala

1 5 10

15

Gln Val Ile Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu

20 25

30

Asp Val Val Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr

35 40

45

Val Ala Thr Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp

50 55

60

Pro Val Leu Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr

65 70

75

80

Asp Thr Ala Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr

85

90

95

Pro Asn Asn Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu
 100 105 110

Thr Ile Asp Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly
 115 120 125

Pro Gln Tyr Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn
 130 135 140

Ala Val Asp Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu
 145 150 155 160

Pro Lys Ile Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala
 165 170 175

Ala Val Ile Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala
 180 185 190

Val Thr Thr Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val
 195 200 205

Ala Ser Asn Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys
 210 215 220

<210> 1127

<211> 638

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(615)

<223> FRXA01617

<400> 1127

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 Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val
 1 5 10 15

aag atc ggt atg ttg ggt act cct gca acg atc gat act gtg gca acc 96
 Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr
 20 25 30

gct ttg gag gaa aac agc ttc aag cac gtt gtc cta gac ccg gta ctg 144
 Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu
 35 40 45

atc tgc aag ggc cag gag ccc ggc gcg gca ctt gat act gac act gcc 192
 Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala
 50 55 60

ctt cgc gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac 240
 Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn
 65 70 75 80

ttc gag gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac	288
Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp	
85	90
95	
gac ctg aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac	336
Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr	
100	105
110	
gtc gtt gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac	384
Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp	
115	120
125	
gta ctt ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc	432
Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile	
130	135
140	
ggc gac gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc	480
Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile	
145	150
155	160
acc gca gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc	528
Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr	
165	170
175	
gct aag cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac	576
Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn	
180	185
190	
gca ccg ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt	625
Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys	
195	200
205	
aaacaagctc cct	638

<210> 1128

<211> 205

<212> PRT

<213> Corynebacterium glutamicum

<400> 1128

Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val	
1	5
10	15

Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr	
20	25
30	

Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu	
35	40
45	

Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala	
50	55
60	

Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn	
65	70
75	80

Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp	
85	90
95	

Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr	
100	105
110	

Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp
 115 120 125

Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile
 130 135 140

Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile
 145 150 155 160

Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr
 165 170 175

Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn
 180 185 190

Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys
 195 200 205

<210> 1129

<211> 792

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(769)

<223> RXC01600

<400> 1129

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tttggagctg cgtgtccacc ctttagatcta caatgtgatc atg gtt tcg aag atg 115
 Met Val Ser Lys Met
 1 5

cac att ccc ggt acc cat gag ttc acg gtg aca gat act gaa ctg ttg 163
 His Ile Pro Gly Thr His Glu Phe Thr Val Thr Asp Thr Glu Leu Leu
 10 15 20

tta gag tcc cca att ttg ggc gtt cgt cga gat tca ttg atc atg ccg 211
 Leu Glu Ser Pro Ile Leu Gly Val Arg Arg Asp Ser Leu Ile Met Pro
 25 30 35

ggt ggt tcc act gcc cgc cgt gaa gtg gtt gaa cac ttt ggg gcg gtc 259
 Gly Gly Ser Thr Ala Arg Arg Glu Val Val Glu His Phe Gly Ala Val
 40 45 50

gca gtg gtt gcc ttt gat ggt gaa aac att gcg atg gtc aag cag tac 307
 Ala Val Val Ala Phe Asp Gly Glu Asn Ile Ala Met Val Lys Gln Tyr
 55 60 65

cgt cgc agc gtg ggg gat tcc ttg tgg gag ctg cct gca ggt ttg ttg 355
 Arg Arg Ser Val Gly Asp Ser Leu Trp Glu Leu Pro Ala Gly Leu Leu
 70 75 80 85

gat att gct gat gag gat gaa ctc acg ggc gcg cag cgc gag ctc atg 403
 Asp Ile Ala Asp Glu Asp Glu Leu Thr Gly Ala Gln Arg Glu Leu Met
 90 95 100

gag gag gct ggt ttg gag gcc agt gag tgg tcc gtg ctc act gat ttg	451
Glu Glu Ala Gly Leu Glu Ala Ser Glu Trp Ser Val Leu Thr Asp Leu	
105	110
115	
att acc tcg cct ggt ttc tgc gat gaa gcg gtg cgt gtc ttt cta gcc	499
Ile Thr Ser Pro Gly Phe Cys Asp Glu Ala Val Arg Val Phe Leu Ala	
120	125
130	
cga ggc ctc aca aag gtt gag cgc ccg aag gtt atg ggc gat gaa gaa	547
Arg Gly Leu Thr Lys Val Glu Arg Pro Lys Val Met Gly Asp Glu Glu	
135	140
145	
gcg gac atg att aac cag tgg gtt ccg cta cat gag gca gtg gga atg	595
Ala Asp Met Ile Asn Gln Trp Val Pro Leu His Glu Ala Val Gly Met	
150	155
160	165
gtg ttt agt ggc cag ttg gtt aac tcc att gcc att gcg ggt gtc atg	643
Val Phe Ser Gly Gln Leu Val Asn Ser Ile Ala Ile Ala Gly Val Met	
170	175
180	
gct gct gat gct gtg att gcg ggt cgt gcg tct gcg cgt gcc gtc acc	691
Ala Ala Asp Ala Val Ile Ala Gly Arg Ala Ser Ala Arg Ala Val Thr	
185	190
195	
gcg ccg ttt acc tat cgc cct acg gcg ttg gcg cag cgt cga aaa gcg	739
Ala Pro Phe Thr Tyr Arg Pro Thr Ala Leu Ala Gln Arg Arg Lys Ala	
200	205
210	
cac ggc att gtt cct gac atg aaa aaa cta tgaaggctcg cgtttagcg	789
His Gly Ile Val Pro Asp Met Lys Lys Leu	
215	220
aaa	792

<210> 1130

<211> 223

<212> PRT

<213> Corynebacterium glutamicum

<400> 1130

Met Val Ser Lys Met His Ile Pro Gly Thr His Glu Phe Thr Val Thr	
1	5
10	15

Asp Thr Glu Leu Leu Glu Ser Pro Ile Leu Gly Val Arg Arg Asp	
20	25
30	

Ser Leu Ile Met Pro Gly Gly Ser Thr Ala Arg Arg Glu Val Val Glu	
35	40
45	

His Phe Gly Ala Val Ala Val Ala Phe Asp Gly Glu Asn Ile Ala	
50	55
60	

Met Val Lys Gln Tyr Arg Arg Ser Val Gly Asp Ser Leu Trp Glu Leu	
65	70
75	80

Pro Ala Gly Leu Leu Asp Ile Ala Asp Glu Asp Glu Leu Thr Gly Ala	
85	90
95	

Gln Arg Glu Leu Met Glu Glu Ala Gly Leu Glu Ala Ser Glu Trp Ser	
100	105
110	

Val Leu Thr Asp Leu Ile Thr Ser Pro Gly Phe Cys Asp Glu Ala Val
115 120 125

Arg Val Phe Leu Ala Arg Gly Leu Thr Lys Val Glu Arg Pro Lys Val
130 135 140

Met Gly Asp Glu Glu Ala Asp Met Ile Asn Gln Trp Val Pro Leu His
145 150 155 160

Glu Ala Val Gly Met Val Phe Ser Gly Gln Leu Val Asn Ser Ile Ala
165 170 175

Ile Ala Gly Val Met Ala Ala Asp Ala Val Ile Ala Gly Arg Ala Ser
180 185 190

Ala Arg Ala Val Thr Ala Pro Phe Thr Tyr Arg Pro Thr Ala Leu Ala
195 200 205

Gln Arg Arg Lys Ala His Gly Ile Val Pro Asp Met Lys Lys Leu
210 215 220

<210> 1131

<211> 726

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(703)

<223> RXC01622

<400> 1131

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gccatcgca agctgaagag ctgggtggaa ggagaaaaaca atg agt gat ttt tat 115
Met Ser Asp Phe Tyr
1 5

gcc gac agg ttg ttt aac gcg atg gag cgc aat gag gta gct cca ggc 163
Ala Asp Arg Leu Phe Asn Ala Met Glu Arg Asn Glu Val Ala Pro Gly
10 15 20

atg ttg ttg gtg gct gcg ccc gat atg gcg tcg gag gat ttt gag cgc 211
Met Leu Leu Val Ala Ala Pro Asp Met Ala Ser Glu Asp Phe Glu Arg
25 30 35

agc atc gtg ttg atc atc gag cat tct cct gcc acc act ttt ggt gtg 259
Ser Ile Val Leu Ile Ile Glu His Ser Pro Ala Thr Thr Phe Gly Val
40 45 50

aac att tct tca cgt tcc gat gtt gct gtg gcc aat gtg ttg ccc gag 307
Asn Ile Ser Ser Arg Ser Asp Val Ala Val Ala Asn Val Leu Pro Glu
55 60 65

tgg gtg gac ctc acc tcg aag cca cag gca ctg tac atc ggt ggg ccg 355
Trp Val Asp Leu Thr Ser Lys Pro Gln Ala Leu Tyr Ile Gly Gly Pro
70 75 80 85

ttg agc cag cag gct gtg gtt ggt ttg ggc gtg acc aag ccg ggc gtg 403

Leu Ser Gln Gln Ala Val Val Gly Leu Gly Val Thr Lys Pro Gly Val			
90	95	100	
gat att gaa aat tcc acc agc ttc aac aag ctc gcc aac cgc ctg gtg			451
Asp Ile Glu Asn Ser Thr Ser Phe Asn Lys Leu Ala Asn Arg Leu Val			
105	110	115	
cac gtg gat ctg cgt tct gca cct gaa gat gtg gct gat gat ctt gag			499
His Val Asp Leu Arg Ser Ala Pro Glu Asp Val Ala Asp Asp Leu Glu			
120	125	130	
ggc atg cgc ttt ttt gcg ggc tac gcg gag tgg gct ccg ggc cag ctc			547
Gly Met Arg Phe Phe Ala Gly Tyr Ala Glu Trp Ala Pro Gly Gln Leu			
135	140	145	
aac gag gaa att gag cag ggt gat tgg ttc gtc aca cct gcg ttg ccg			595
Asn Glu Glu Ile Glu Gln Gly Asp Trp Phe Val Thr Pro Ala Leu Pro			
150	155	160	165
tcg gac att atc gcg ccg ggc cgc gtc gat att tgg ggc gac gtg atg			643
Ser Asp Ile Ile Ala Pro Gly Arg Val Asp Ile Trp Gly Asp Val Met			
170	175	180	
cgt cga caa gca atg cct ttg ccg ttg tat tcc acg ttt ccg tcg gac			691
Arg Arg Gln Ala Met Pro Leu Pro Leu Tyr Ser Thr Phe Pro Ser Asp			
185	190	195	
cct tca gat aat tagatgagtt ccgaaaattt aaa			726
Pro Ser Asp Asn			
200			
<210> 1132			
<211> 201			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 1132			
Met Ser Asp Phe Tyr Ala Asp Arg Leu Phe Asn Ala Met Glu Arg Asn			
1	5	10	15
Glu Val Ala Pro Gly Met Leu Leu Val Ala Ala Pro Asp Met Ala Ser			
20	25	30	
Glu Asp Phe Glu Arg Ser Ile Val Leu Ile Ile Glu His Ser Pro Ala			
35	40	45	
Thr Thr Phe Gly Val Asn Ile Ser Ser Arg Ser Asp Val Ala Val Ala			
50	55	60	
Asn Val Leu Pro Glu Trp Val Asp Leu Thr Ser Lys Pro Gln Ala Leu			
65	70	75	80
Tyr Ile Gly Gly Pro Leu Ser Gln Gln Ala Val Val Gly Leu Gly Val			
85	90	95	
Thr Lys Pro Gly Val Asp Ile Glu Asn Ser Thr Ser Phe Asn Lys Leu			
100	105	110	
Ala Asn Arg Leu Val His Val Asp Leu Arg Ser Ala Pro Glu Asp Val			
115	120	125	

Ala Asp Asp Leu Glu Gly Met Arg Phe Phe Ala Gly Tyr Ala Glu Trp
 130 135 140

Ala Pro Gly Gln Leu Asn Glu Glu Ile Glu Gln Gly Asp Trp Phe Val
 145 150 155 160

Thr Pro Ala Leu Pro Ser Asp Ile Ile Ala Pro Gly Arg Val Asp Ile
 165 170 175

Trp Gly Asp Val Met Arg Arg Gln Ala Met Pro Leu Pro Leu Tyr Ser
 180 185 190

Thr Phe Pro Ser Asp Pro Ser Asp Asn
 195 200

<210> 1133

<211> 1827

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1804)

<223> RXC00128

<400> 1133

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cgttgcgcgc tccagagaca ccgtggaaag gggagcagca gtg agt aaa att tcg 115
 Val Ser Lys Ile Ser
 1 5

acg aaa ctg aag gcc ctc acc gcg gtg ctg tct gtg acc act ctg gtg 163
 Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser Val Thr Thr Leu Val
 10 15 20

gct ggg tgt tcc acg ctt ccg cag aac acg gat ccg caa gtg ctg cgc 211
 Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp Pro Gln Val Leu Arg
 25 30 35

tca ttt tcc ggg tcc caa agc aca caa gag ata gca ggg ccg acc ccg 259
 Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile Ala Gly Pro Thr Pro
 40 45 50

aat caa gat ccg gat ttg ttg atc cgc ggc ttc ttc agc gca ggt gcg 307
 Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe Phe Ser Ala Gly Ala
 55 60 65

tat ccg act cag cag tat gaa gcg gcg aag gcg tat ctg acg gaa ggg 355
 Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala Tyr Leu Thr Glu Gly
 70 75 80 85

acg cgc agc acg tgg aat ccg gct gcg tcg act cgt att ttg gat cgc 403
 Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr Arg Ile Leu Asp Arg
 90 95 100

att gat ctg aac act ctg cca ggt tcg acg aat gcg gaa cga acg att 451
 Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn Ala Glu Arg Thr Ile
 105 110 115

gct atc cgt gga acg cag gtc gga acg ttg ctc agc ggt ggc gtg tat	499
Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu Ser Gly Gly Val Tyr	
120	125
130	
cag ccg gag aat gct gag ttt gaa gct gag atc acg atg cgt cgaa gaa	547
Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile Thr Met Arg Arg Glu	
135	140
145	
gat ggg gag tgg cgt atc gat gct ttg ccg gac ggg att tta tta gag	595
Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp Gly Ile Leu Leu Glu	
150	155
160	165
aga aac gat ctg cgg aac cat tac act ccg cac gat gtg tat ttc ttt	643
Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His Asp Val Tyr Phe Phe	
170	175
180	
gat cct tct ggc cag gtg ttg gtg ggg gat ccg cgt tgg ttg ttc aat	691
Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg Arg Trp Leu Phe Asn	
185	190
195	
gag tcg cag tcg atg tcc acg gtg ctg atg gcc ctt ctg gtt aat ggt	739
Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala Leu Leu Val Asn Gly	
200	205
210	
cct tcg ccg gca att tct cct ggt gtg gtc aat cag ctg tcc acg gat	787
Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn Gln Leu Ser Thr Asp	
215	220
225	
gct tcg ttc gtg ggg ttc aat gat ggg gag tat cag ttc act ggt ttg	835
Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr Gln Phe Thr Gly Leu	
230	235
240	245
gga aat ttg gat gat gat gct cgt ttg cgt ttc gcc gcc cag gcc gtg	883
Gly Asn Leu Asp Asp Ala Arg Leu Arg Phe Ala Ala Gln Ala Val	
250	255
260	
tgg acg ttg gcg cat gct gat gtc gca ggc ccc tac act ttg gtc gct	931
Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro Tyr Thr Leu Val Ala	
265	270
275	
gac ggc gcg ccg ttg ctg tcg gag ttc cca acg ctc acc acc gat gac	979
Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr Leu Thr Thr Asp Asp	
280	285
290	
ctc gcc gaa tac aac cca gag gct tac acc aac acg gtg tcc acg ttg	
1027	
Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn Thr Val Ser Thr Leu	
295	300
305	
ttt gct ttg cag gat gga tcg ttg tcg agg gtc agt tcc ggc aat gtg	
1075	
Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val Ser Ser Gly Asn Val	
310	315
320	325
agt cca cta cag ggc att tgg agc ggt gga gat atc gat tct gca gcg	
1123	
Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp Ile Asp Ser Ala Ala	
330	335
340	

att tcc tcc tcc gcc aat gtg gtg gca gcg gta cgc cac gaa aac aac
1171
Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val Arg His Glu Asn Asn
345 350 355

gag gca gtg ctt act gtt ggc tcc atg gaa ggc gtg act tca gat gcg
1219
Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly Val Thr Ser Asp Ala
360 365 370

ttg agg agt gaa acg atc act cgt ccc acc ttt gaa tac gcg tcg agt
1267
Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe Glu Tyr Ala Ser Ser
375 380 385

ggg ttg tgg gct gtg gtg gat ggg gag acg cct gtc cga gtc gca cga
1315
Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro Val Arg Val Ala Arg
390 395 400 405

tcg gca aca acc ggt gag ctc gtc cag acg gag gcg gag att gtg ctg
1363
Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu Ala Glu Ile Val Leu
410 415 420

cca agg gat gtg acg ggt ccg atc tct gaa ttc caa ctg tca cga act
1411
Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe Gln Leu Ser Arg Thr
425 430 435

ggg gtc cgg gcc gcc atg atc att gaa ggc aag gtg tac gtg ggc gtc
1459
Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys Val Tyr Val Gly Val
440 445 450

gta acg cgt cct ggt ccg ggc gag cgg cgc gtg aca aat atc acg gag
1507
Val Thr Arg Pro Gly Pro Glu Arg Arg Val Thr Asn Ile Thr Glu
455 460 465

gtg gcg ccg agc ttg ggc gag gcg gcg ctg tcg atc aac tgg cgc cca
1555
Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser Ile Asn Trp Arg Pro
470 475 480 485

gac ggc att ttg ctt gtg ggc acg tca att cca gag acg ccg ctg tgg
1603
Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp
490 495 500

cgc gtc gag cag gac gga tcg gcg att tcg tcg atg ccg agc ggg aat
1651
Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn
505 510 515

ctc agc gcg ccg gtg gtg gcg gtg gca agt tcc gcg acg acg gtc tac
1699
Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr
520 525 530

gtc act gat tcg cat gcg atg ctt cag ctg ccg act gcc gat aat gat
 1747
 Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp
 535 540 545

att tgg cgc gag gtg ccc ggt ttg ctg ggc acg cgt gcg gcg ccg gtg
 1795
 Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr Arg Ala Ala Pro Val
 550 555 560 565

gtt gcg tac tgatggagct gttcttccccg cgc
 1827
 Val Ala Tyr

<210> 1134
<211> 568
<212> PRT
<213> Corynebacterium glutamicum

<400> 1134
Val Ser Lys Ile Ser Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser
 1 5 10 15

Val Thr Thr Leu Val Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp
 20 25 30

Pro Gln Val Leu Arg Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile
 35 40 45

Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe
 50 55 60

Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala
 65 70 75 80

Tyr Leu Thr Glu Gly Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr
 85 90 95

Arg Ile Leu Asp Arg Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn
 100 105 110

Ala Glu Arg Thr Ile Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu
 115 120 125

Ser Gly Gly Val Tyr Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile
 130 135 140

Thr Met Arg Arg Glu Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp
 145 150 155 160

Gly Ile Leu Leu Glu Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His
 165 170 175

Asp Val Tyr Phe Phe Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg
 180 185 190

Arg Trp Leu Phe Asn Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala
 195 200 205

Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn
210 215 220

Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr
225 230 235 240

Gln Phe Thr Gly Leu Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe
245 250 255

Ala Ala Gln Ala Val Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro
260 265 270

Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr
275 280 285

Leu Thr Thr Asp Asp Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn
290 295 300

Thr Val Ser Thr Leu Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val
305 310 315 320

Ser Ser Gly Asn Val Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp
325 330 335

Ile Asp Ser Ala Ala Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val
340 345 350

Arg His Glu Asn Asn Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly
355 360 365

Val Thr Ser Asp Ala Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe
370 375 380

Glu Tyr Ala Ser Ser Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro
385 390 395 400

Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu
405 410 415

Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe
420 425 430

Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys
435 440 445

Val Tyr Val Gly Val Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val
450 455 460

Thr Asn Ile Thr Glu Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser
465 470 475 480

Ile Asn Trp Arg Pro Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro
485 490 495

Glu Thr Pro Leu Trp Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser
500 505 510

Met Pro Ser Gly Asn Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser
515 520 525

Ala Thr Thr Val Tyr Val Thr Asp Ser His Ala Met Leu Gln Leu Pro

530

535

540

Thr Ala Asp Asn Asp Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr
 545 550 555 560

Arg Ala Ala Pro Val Val Ala Tyr
 565

<210> 1135

<211> 555

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(532)

<223> RXC01709

<400> 1135

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gaaatttagt gtcgatgcag caatacggaa ctttgc当地 gtg ttt gaa caa gct 115
 Val Phe Glu Gln Ala
 1 5

ctc ggg ctc acc acc ctt gca caa aca gct gga gcg ggc gca gcg ggg 163
 Leu Gly Leu Thr Thr Leu Ala Gln Thr Ala Gly Ala Gly Ala Gly
 10 15 20

ggc ttg ggt ttc atg gca atg gcg ttg ttg tct gca ggg atg cgc tcc 211
 Gly Leu Gly Phe Met Ala Met Ala Leu Leu Ser Ala Gly Met Arg Ser
 25 30 35

ggc gtg gac atg att ctt aat gaa acc ggg ggt gaa aag atg ctt gca 259
 Gly Val Asp Met Ile Leu Asn Glu Thr Gly Gly Glu Lys Met Leu Ala
 40 45 50

cag gca gat tta gtc atc act gga gaa gga cgc att gat gca cag acc 307
 Gln Ala Asp Leu Val Ile Thr Gly Glu Gly Arg Ile Asp Ala Gln Thr
 55 60 65

ctc agc ggg aaa gct cct act gga atc gcc aaa cgg gca cgt gcg aaa 355
 Leu Ser Gly Lys Ala Pro Thr Gly Ile Ala Lys Arg Ala Arg Ala Lys
 70 75 80 85

gga att cca gta ctg gcg gtt tgt ggg cag agc cta ttg ggt cca gca 403
 Gly Ile Pro Val Leu Ala Val Cys Gly Gln Ser Leu Leu Gly Pro Ala
 90 95 100

atc tca aat gag cta ttt gaa gac atc tac agc ttt acc gat ttc gaa 451
 Ile Ser Asn Glu Leu Phe Glu Asp Ile Tyr Ser Phe Thr Asp Phe Glu
 105 110 115

tct gac atc aat gaa tgc att cga aac ccg ctc cca att ttg gaa ggt 499
 Ser Asp Ile Asn Glu Cys Ile Arg Asn Pro Leu Pro Ile Leu Glu Gly
 120 125 130

atc ggt ttt aac atc gcc aaa cat cat ctg agt tagcgatatt tcagcaaacc 552
 Ile Gly Phe Asn Ile Ala Lys His His Leu Ser
 135 140

gat

555

<210> 1136
<211> 144
<212> PRT
<213> Corynebacterium glutamicum

<400> 1136

Val	Phe	Glu	Gln	Ala	Leu	Gly	Leu	Thr	Thr	Leu	Ala	Gln	Thr	Ala	Gly
1				5				10					15		

Ala Gly Ala Ala Gly Gly Leu Gly Phe Met Ala Met Ala Leu Leu Ser

	20				25					30					
--	----	--	--	--	----	--	--	--	--	----	--	--	--	--	--

Ala Gly Met Arg Ser Gly Val Asp Met Ile Leu Asn Glu Thr Gly Gly

	35				40				45						
--	----	--	--	--	----	--	--	--	----	--	--	--	--	--	--

Glu Lys Met Leu Ala Gln Ala Asp Leu Val Ile Thr Gly Glu Gly Arg

	50				55			60							
--	----	--	--	--	----	--	--	----	--	--	--	--	--	--	--

Ile Asp Ala Gln Thr Leu Ser Gly Lys Ala Pro Thr Gly Ile Ala Lys

	65				70			75		80					
--	----	--	--	--	----	--	--	----	--	----	--	--	--	--	--

Arg Ala Arg Ala Lys Gly Ile Pro Val Leu Ala Val Cys Gly Gln Ser

	85				90				95.						
--	----	--	--	--	----	--	--	--	-----	--	--	--	--	--	--

Leu Leu Gly Pro Ala Ile Ser Asn Glu Leu Phe Glu Asp Ile Tyr Ser

	100				105				110						
--	-----	--	--	--	-----	--	--	--	-----	--	--	--	--	--	--

Phe Thr Asp Phe Glu Ser Asp Ile Asn Glu Cys Ile Arg Asn Pro Leu

	115				120			125							
--	-----	--	--	--	-----	--	--	-----	--	--	--	--	--	--	--

Pro Ile Leu Glu Gly Ile Gly Phe Asn Ile Ala Lys His His Leu Ser

	130				135			140							
--	-----	--	--	--	-----	--	--	-----	--	--	--	--	--	--	--

<210> 1137
<211> 898
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(898)
<223> RXC02207

<400> 1137

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ggtccaatta	cattcaactgg	taatctgaaa	ccttgtgaat	atg	cgc	cgt	cga	tcc	115
					Met	Arg	Arg	Ser	
					1			5	

cgt gtg tcc cgt ttg ctt ccc gcc aca gct ttg ctg gcc tca act gca 163

Arg	Val	Ser	Arg	Leu	Leu	Pro	Ala	Thr	Ala	Leu	Leu	Ala	Ser	Thr	Ala
				10				15					20		

ctt ctt tta agt gca tgt acg caa ggg gta acg gac tcc ccg gat atg	211		
Leu Leu Leu Ser Ala Cys Thr Gln Gly Val Thr Asp Ser Pro Asp Met			
25	30	35	
ggc aag gca act ccc gct gtc tcc ccc gca gca agc aac ccg gat ggc	259		
Gly Lys Ala Thr Pro Ala Val Ser Pro Ala Ala Ser Asn Pro Asp Gly			
40	45	50	
caa gta att gag ttc ggc aac atc act gac atg gaa gtc act gat ggt	307		
Gln Val Ile Glu Phe Gly Asn Ile Thr Asp Met Glu Val Thr Asp Gly			
55	60	65	
gac atc ctc ggt gta cgc acc gaa gac gca ctc gct att ggt aca gtc	355		
Asp Ile Leu Gly Val Arg Thr Glu Asp Ala Leu Ala Ile Gly Thr Val			
70	75	80	85
tcc gac ttc gaa gcg ggt agc cag gtg gaa ctg gac gtc gat aag caa	403		
Ser Asp Phe Glu Ala Gly Ser Gln Val Glu Leu Asp Val Asp Lys Gln			
90	95	100	
tgc ggc gac ctg acc gca acc ggc ggc act ttc gtg ctc ccc tgc gcc	451		
Cys Gly Asp Leu Thr Ala Thr Gly Gly Thr Phe Val Leu Pro Cys Ala			
105	110	115	
gat ggc gtt tat ttg att gat gcc aag gac ccg gat ctg gat gag ttg	499		
Asp Gly Val Tyr Leu Ile Asp Ala Lys Asp Pro Asp Leu Asp Glu Leu			
120	125	130	
cgt gca act gac aag cca gtc acg gtg gca gcc ttg acc agc gat gat	547		
Arg Ala Thr Asp Lys Pro Val Thr Val Ala Ala Leu Thr Ser Asp Asp			
135	140	145	
cag ctt ctg gtg ggc aat ggt gaa gat gaa gaa ctc acc atc tac cgc	595		
Gln Leu Leu Val Gly Asn Gly Glu Asp Glu Glu Leu Thr Ile Tyr Arg			
150	155	160	165
gag ggc gaa gag cca gaa acc ttc acc gtc gcg ggt ccc aat acc cag	643		
Glu Gly Glu Glu Pro Glu Thr Phe Thr Val Ala Gly Pro Asn Thr Gln			
170	175	180	
ctc atc gcc gtt cct gtc att gat cgc cac gac gcc gtt gtg cgc acc	691		
Leu Ile Ala Val Pro Val Ile Asp Arg His Asp Ala Val Val Arg Thr			
185	190	195	
tgg aac gaa aac acc acg att caa gat gtg gac tac ccc aac gac cgt	739		
Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp Tyr Pro Asn Asp Arg			
200	205	210	
gaa ggc gcg acc ctt cgc gtg gga ctc ggc gtt ggt caa atg gct ggt	787		
Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val Gly Gln Met Ala Gly			
215	220	225	
ggc gaa gac ggc ctg ctg gtg gtc tct gat gaa atg ggt ggc caa att	835		
Gly Glu Asp Gly Leu Leu Val Val Ser Asp Glu Met Gly Gly Gln Ile			
230	235	240	245
gcc atc tac aac gct gat gat gtc atc cga ctt caa aat gac cgc ccc	883		
Ala Ile Tyr Asn Ala Asp Asp Val Ile Arg Leu Gln Asn Asp Arg Pro			
250	255	260	

cac cga cga gga acc
 His Arg Arg Gly Thr
 265

898

<210> 1138

<211> 266

<212> PRT

<213> Corynebacterium glutamicum

<400> 1138

Met	Arg	Arg	Arg	Ser	Arg	Val	Ser	Arg	Leu	Leu	Pro	Ala	Thr	Ala	Leu
1				5				10					15		

Leu	Ala	Ser	Thr	Ala	Leu	Leu	Ser	Ala	Cys	Thr	Gln	Gly	Val	Thr
				20			25				30			

Asp	Ser	Pro	Asp	Met	Gly	Lys	Ala	Thr	Pro	Ala	Val	Ser	Pro	Ala	Ala
				35			40					45			

Ser	Asn	Pro	Asp	Gly	Gln	Val	Ile	Glu	Phe	Gly	Asn	Ile	Thr	Asp	Met
					50		55				60				

Glu	Val	Thr	Asp	Gly	Asp	Ile	Leu	Gly	Val	Arg	Thr	Glu	Asp	Ala	Leu
					65		70		75		80				

Ala	Ile	Gly	Thr	Val	Ser	Asp	Phe	Glu	Ala	Gly	Ser	Gln	Val	Glu	Leu
				85				90				95			

Asp	Val	Asp	Lys	Gln	Cys	Gly	Asp	Leu	Thr	Ala	Thr	Gly	Gly	Thr	Phe
				100			105				110				

Val	Leu	Pro	Cys	Ala	Asp	Gly	Val	Tyr	Leu	Ile	Asp	Ala	Lys	Asp	Pro
				115			120			125					

Asp	Leu	Asp	Glu	Leu	Arg	Ala	Thr	Asp	Lys	Pro	Val	Thr	Val	Ala	Ala
					130		135			140					

Leu	Thr	Ser	Asp	Asp	Gln	Leu	Leu	Val	Gly	Asn	Gly	Glu	Asp	Glu	Glu
					145		150		155		160				

Leu	Thr	Ile	Tyr	Arg	Glu	Gly	Glu	Pro	Glu	Thr	Phe	Thr	Val	Ala
				165			170			175				

Gly	Pro	Asn	Thr	Gln	Leu	Ile	Ala	Val	Pro	Val	Ile	Asp	Arg	His	Asp
				180			185			190					

Ala	Val	Val	Arg	Thr	Trp	Asn	Glu	Asn	Thr	Thr	Ile	Gln	Asp	Val	Asp
				195			200			205					

Tyr	Pro	Asn	Asp	Arg	Glu	Gly	Ala	Thr	Leu	Arg	Val	Gly	Leu	Gly	Val
				210			215			220					

Gly	Gln	Met	Ala	Gly	Gly	Glu	Asp	Gly	Leu	Leu	Val	Val	Ser	Asp	Glu
				225			230		235			240			

Met	Gly	Gly	Gln	Ile	Ala	Ile	Tyr	Asn	Ala	Asp	Asp	Val	Ile	Arg	Leu
				245			250			255					

Gln	Asn	Asp	Arg	Pro	His	Arg	Arg	Gly	Thr
				260			265		

<210> 1139
 <211> 891
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(868)
 <223> RXA00347

<400> 1139
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 aaagtgccag gggttctgtg ggatccgtac actggttccc atg act ttg act att 115
 Met Thr Leu Thr Ile
 1 5

gag gaa atc gcc aag acc aaa aag ctt ttg gtt gtg tcc gat ttt gat 163
 Glu Glu Ile Ala Lys Thr Lys Lys Leu Leu Val Val Ser Asp Phe Asp
 10 15 20

gga acc atc gca gga ttt agc aag gac gct tac aac gtt cct atc aac 211
 Gly Thr Ile Ala Gly Phe Ser Lys Asp Ala Tyr Asn Val Pro Ile Asn
 25 30 35

cag aaa tcc ctc aag gcg gta aaa gac ctc tcc caa caa gca gac act 259
 Gln Lys Ser Leu Lys Ala Val Lys Asp Leu Ser Gln Gln Ala Asp Thr
 40 45 50

gat gtt gtc att ttg tcg gga cgt cac ctg gag gga ttg aag acg gtt 307
 Asp Val Val Ile Leu Ser Gly Arg His Leu Glu Gly Leu Lys Thr Val
 55 60 65

ctt gat ctt ggt cag tac gac atc acc atg gtg ggt tca cac ggt tct 355
 Leu Asp Leu Gly Gln Tyr Asp Ile Thr Met Val Gly Ser His Gly Ser
 70 75 80 85

gag gat tcc tcc cgc ccg cgt acc ctc act cct gaa gag gta gct cgc 403
 Glu Asp Ser Ser Arg Pro Arg Thr Leu Thr Pro Glu Glu Val Ala Arg
 90 95 100

ctc gcc aag att gaa gca gat ctg gaa aag atc gtc gac ggc atc gaa 451
 Leu Ala Lys Ile Glu Ala Asp Leu Glu Lys Ile Val Asp Gly Ile Glu
 105 110 115

ggc gca ttc gtg gag atc aag cct ttc cac cgc gtg ctg cac ttc atc 499
 Gly Ala Phe Val Glu Ile Lys Pro Phe His Arg Val Leu His Phe Ile
 120 125 130

cgt gtt tcc gac aag gac aaa gtc caa gga atc ctc gcc caa gca gca 547
 Arg Val Ser Asp Lys Asp Lys Val Gln Gly Ile Leu Ala Gln Ala Ala
 135 140 145

cac gta gac tct tcc ggc ctg aag gtt act aac ggc aag agc atc atc 595
 His Val Asp Ser Ser Gly Leu Lys Val Thr Asn Gly Lys Ser Ile Ile
 150 155 160 165

gaa tac tcc atc agc tcc acc acc aag ggc acc tgg ctg aag gaa tac 643
 Glu Tyr Ser Ile Ser Ser Thr Thr Lys Gly Thr Trp Leu Lys Glu Tyr

170

175

180

gtt gac cgc acc gag ccc act ggt gtg att ttc ctc ggc gat gac acc 691
 Val Asp Arg Thr Glu Pro Thr Gly Val Ile Phe Leu Gly Asp Asp Thr
 185 190 195

acc gat gag cac ggt ttc aaa gct tta gaa aac gat gat cgt gcc cta 739
 Thr Asp Glu His Gly Phe Lys Ala Leu Glu Asn Asp Asp Arg Ala Leu
 200 205 210

acc gtc aag gtt ggc gaa gga gac act gca gcc aaa acc cgc gtc gac 787
 Thr Val Lys Val Gly Glu Gly Asp Thr Ala Ala Lys Thr Arg Val Asp
 215 220 225

gat gtt gat aat gtg gga att ttc cta gag aaa ctc gcc tac cac cgc 835
 Asp Val Asp Asn Val Gly Ile Phe Leu Glu Lys Leu Ala Tyr His Arg
 230 235 240 245

atg cag tat gcg gaa agc gtg cga ttg ggg att taagagagcc taaaacgcacg 888
 Met Gln Tyr Ala Glu Ser Val Arg Leu Gly Ile
 250 255

aaa 891

<210> 1140

<211> 256

<212> PRT

<213> Corynebacterium glutamicum

<400> 1140

Met Thr Leu Thr Ile Glu Glu Ile Ala Lys Thr Lys Lys Leu Leu Val
 1 5 10 15

Val Ser Asp Phe Asp Gly Thr Ile Ala Gly Phe Ser Lys Asp Ala Tyr
 20 25 30

Asn Val Pro Ile Asn Gln Lys Ser Leu Lys Ala Val Lys Asp Leu Ser
 35 40 45

Gln Gln Ala Asp Thr Asp Val Val Ile Leu Ser Gly Arg His Leu Glu
 50 55 60

Gly Leu Lys Thr Val Leu Asp Leu Gly Gln Tyr Asp Ile Thr Met Val
 65 70 75 80

Gly Ser His Gly Ser Glu Asp Ser Ser Arg Pro Arg Thr Leu Thr Pro
 85 90 95

Glu Glu Val Ala Arg Leu Ala Lys Ile Glu Ala Asp Leu Glu Lys Ile
 100 105 110

Val Asp Gly Ile Glu Gly Ala Phe Val Glu Ile Lys Pro Phe His Arg
 115 120 125

Val Leu His Phe Ile Arg Val Ser Asp Lys Asp Lys Val Gln Gly Ile
 130 135 140

Leu Ala Gln Ala Ala His Val Asp Ser Ser Gly Leu Lys Val Thr Asn
 145 150 155 160

Gly Lys Ser Ile Ile Glu Tyr Ser Ile Ser Ser Thr Thr Lys Gly Thr
 165 170 175

Trp Leu Lys Glu Tyr Val Asp Arg Thr Glu Pro Thr Gly Val Ile Phe
 180 185 190

Leu Gly Asp Asp Thr Thr Asp Glu His Gly Phe Lys Ala Leu Glu Asn
 195 200 205

Asp Asp Arg Ala Leu Thr Val Lys Val Gly Glu Gly Asp Thr Ala Ala
 210 215 220

Lys Thr Arg Val Asp Asp Val Asp Asn Val Gly Ile Phe Leu Glu Lys
 225 230 235 240

Leu Ala Tyr His Arg Met Gln Tyr Ala Glu Ser Val Arg Leu Gly Ile
 245 250 255

<210> 1141

<211> 2556

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2533)

<223> RXN01239

<400> 1141

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gtaccgcacg atttgccta acttttaagg gtgtttcatc atg gca cgt cca att 115
 Met Ala Arg Pro Ile
 1 5

tcc gca acg tac agg ctt caa atg cga gga cct caa gca gat agc gcc 163
 Ser Ala Thr Tyr Arg Leu Gln Met Arg Gly Pro Gln Ala Asp Ser Ala
 10 15 20

ggg cgt tca ttt ggt ttt gcg cag gcc aaa gcc cag ctt ccc tat ctg 211
 Gly Arg Ser Phe Gly Phe Ala Gln Ala Lys Ala Gln Leu Pro Tyr Leu
 25 30 35

aag aag cta ggc atc agc cac ctg tac ctc tcc cct att ttt acg gcc 259
 Lys Lys Leu Gly Ile Ser His Leu Tyr Leu Ser Pro Ile Phe Thr Ala
 40 45 50

atg cca gat tcc aat cat ggc tac gat gtc att gat ccc acc acc atc 307
 Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile Asp Pro Thr Thr Ile
 55 60 65

aat gaa gag ctc ggt ggc atg gag ggt ctt cga gat ctt gcc gca gct 355
 Asn Glu Glu Leu Gly Gly Met Glu Gly Leu Arg Asp Leu Ala Ala Ala
 70 75 80 85

aca cac gag ttg ggc atg ggc atc atc att gat att gtt ccc aac cat 403
 Thr His Glu Leu Gly Met Gly Ile Ile Asp Ile Val Pro Asn His

	90	95	100	
tta ggt gtt gcc gtt cca cat ttg aat cct tgg tgg tgg gat gtt cta Leu Gly Val Ala Val Pro His Leu Asn Pro Trp Trp Trp Asp Val Leu	105	110	115	451
aaa aac ggc aaa gat tcc gct ttt gag ttc tat ttc gat att gac tgg Lys Asn Gly Lys Asp Ser Ala Phe Glu Phe Tyr Phe Asp Ile Asp Trp	120	125	130	499
cac gaa gac aac ggt tct ggt ggc aag ctg ggc atg ccg att ctg ggt His Glu Asp Asn Gly Ser Gly Gly Lys Leu Gly Met Pro Ile Leu Gly	135	140	145	547
gct gaa ggc gat gaa gac aag ctg gaa ttc gcg gag ctt gat gga gag Ala Glu Gly Asp Glu Asp Lys Leu Glu Phe Ala Glu Leu Asp Gly Glu	150	155	160	595
aaa gtg ctc aaa tat ttt gac cac ctc ttc cca atc gcg cct ggt acc Lys Val Leu Lys Tyr Phe Asp His Leu Phe Pro Ile Ala Pro Gly Thr	170	175	180	643
gaa gaa ggg aca ccg caa gaa gtc tac aag cgc cag cat tac cgc ctg Glu Glu Gly Thr Pro Gln Glu Val Tyr Lys Arg Gln His Tyr Arg Leu	185	190	195	691
cag ttc tgg cgc gat ggc gtg atc aac ttc cgt cgc ttc ttt tcc gtg Gln Phe Trp Arg Asp Gly Val Ile Asn Phe Arg Arg Phe Phe Ser Val	200	205	210	739
aat acg ttg gct ggc atc agg caa gaa gat ccc tta gtg ttt gaa cat Asn Thr Leu Ala Gly Ile Arg Gln Glu Asp Pro Leu Val Phe Glu His	215	220	225	787
act cat cgt ctg ctg cgc gaa ttg gtg gcg gaa gac ctc att gac ggc Thr His Arg Leu Leu Arg Glu Leu Val Ala Glu Asp Leu Ile Asp Gly	230	235	240	835
gtg cgc gtc gat cac ccc gac ggg ctt tcc gat cct ttt gga tat ctg Val Arg Val Asp His Pro Asp Gly Leu Ser Asp Pro Phe Gly Tyr Leu	250	255	260	883
cac aga ctc cgc gac ctc att gga cct gac cgc tgg ctg atc atc gaa His Arg Leu Arg Asp Leu Ile Gly Pro Asp Arg Trp Leu Ile Ile Glu	265	270	275	931
aag atc ttg agc gtt gat gaa cca ctc gat ccc cgc ctg gcc gtt gat Lys Ile Leu Ser Val Asp Glu Pro Leu Asp Pro Arg Leu Ala Val Asp	280	285	290	979
ggc acc act ggc tac gac gcc ctc cgt gaa ctc gac ggc gtg ttt atc 1027				
Gly Thr Thr Gly Tyr Asp Ala Leu Arg Glu Leu Asp Gly Val Phe Ile	295	300	305	
tcc cga gaa tct gag gac aaa ttc tcc atg ctg gcg ctg acc cac agt 1075				
Ser Arg Glu Ser Glu Asp Lys Phe Ser Met Leu Ala Leu Thr His Ser	310	315	320	325

gga tcc acc tgg gat gaa cgc gcc ctc aaa tcc acg gag gaa agc ctc
 1123
 Gly Ser Thr Trp Asp Glu Arg Ala Leu Lys Ser Thr Glu Glu Ser Leu
 330 335 340

 aaa cga gtc gtc gcc caa caa gaa ctc gca gcc gaa atc tta agg ctc
 1171
 Lys Arg Val Val Ala Gln Gln Glu Leu Ala Ala Glu Ile Leu Arg Leu
 345 350 355

 gcc cgc gcc atg cgc cgc gat aac ttc tcc acc gca ggc acc aac gtc
 1219
 Ala Arg Ala Met Arg Arg Asp Asn Phe Ser Thr Ala Gly Thr Asn Val
 360 365 370

 acc gaa gac aaa ctt agc gaa acc atc atc gaa tta gtc gcc gcc atg
 1267
 Thr Glu Asp Lys Leu Ser Glu Thr Ile Ile Glu Leu Val Ala Ala Met
 375 380 385

 ccc gtc tac cgc gcc gac tac atc tcc ctc tca cgc acc acc gcc acc
 1315
 Pro Val Tyr Arg Ala Asp Tyr Ile Ser Leu Ser Arg Thr Thr Ala Thr
 390 395 400 405

 gtc atc gcg gag atg tcc aaa cgc ttc ccc tcc cgg cgt gac gca ctc
 1363
 Val Ile Ala Glu Met Ser Lys Arg Phe Pro Ser Arg Arg Asp Ala Leu
 410 415 420

 gac ctc atc gcg gcc ccc ctt ggc aat ggc gag gcc aaa atc cgc
 1411
 Asp Leu Ile Ala Ala Leu Leu Gly Asn Gly Glu Ala Lys Ile Arg
 425 430 435

 ttc gct caa gtc tgc ggc gcc gtc atg gct aaa ggt gtg gaa gac acc
 1459
 Phe Ala Gln Val Cys Gly Ala Val Met Ala Lys Gly Val Glu Asp Thr
 440 445 450

 acc ttc tac cgc gca tct agg ctc gtt gca ttg caa gaa gtc ggt ggc
 1507
 Thr Phe Tyr Arg Ala Ser Arg Leu Val Ala Leu Gln Glu Val Gly Gly
 455 460 465

 gcg ccg ggg aga ttc ggc gtc tcc gct gca gaa ttc cac ttg ctg cag
 1555
 Ala Pro Gly Arg Phe Gly Val Ser Ala Ala Glu Phe His Leu Leu Gln
 470 475 480 485

 gaa gaa cgc agc ctg ctg tgg cca cgc acc atg acc acc ttg tcc acg
 1603
 Glu Glu Arg Ser Leu Leu Trp Pro Arg Thr Met Thr Thr Leu Ser Thr
 490 495 500

 cat gac acc aaa cgt ggc gaa gat acc cgc gcc cgc atc atc tcc ctg
 1651
 His Asp Thr Lys Arg Gly Glu Asp Thr Arg Ala Arg Ile Ile Ser Leu
 505 510 515

tct gaa gtc ccc gat atg tac tcc gag ctg gtc aat cgt gtt ttc gcg
1699 Ser Glu Val Pro Asp Met Tyr Ser Glu Leu Val Asn Arg Val Phe Ala
520 525 530

gtg ctc ccc gcg cca gac ggc gca acg ggc agt ttc ctc cta caa aac
1747 Val Leu Pro Ala Pro Asp Gly Ala Thr Gly Ser Phe Leu Leu Gln Asn
535 540 545

ctg ctg ggc gta tgg ccc gcc gac ggc gtg atc acc gat gcg ctg cgc
1795 Leu Leu Gly Val Trp Pro Ala Asp Gly Val Ile Thr Asp Ala Leu Arg
550 555 560 565

gat cga ttc agg gaa tac gcc cta aaa gct atc cgc gaa gca tcc aca
1843 Asp Arg Phe Arg Glu Tyr Ala Leu Lys Ala Ile Arg Glu Ala Ser Thr
570 575 580

aaa acc acg tgg gtg gac ccc aac gag tcc ttc gag gct gcg gtc tgc
1891 Lys Thr Thr Trp Val Asp Pro Asn Glu Ser Phe Glu Ala Ala Val Cys
585 590 595

gat tgg gtg gaa gcg ctt ttc gac gga ccc tcc acc tca cta atc acc
1939 Asp Trp Val Glu Ala Leu Phe Asp Gly Pro Ser Thr Ser Leu Ile Thr
600 605 610

gaa ttt gtc tcc cac atc aac cgt ggc tct gtg caa atc tcc tta ggc
1987 Glu Phe Val Ser His Ile Asn Arg Gly Ser Val Gln Ile Ser Leu Gly
615 620 625

agg aaa ctg ctg caa atg gtg ggc gct gga atc ccc gac act tac caa
2035 Arg Lys Leu Leu Gln Met Val Gly Ala Gly Ile Pro Asp Thr Tyr Gln
630 635 640 645

gga act gag ttt tta gaa gac tcc ctg gta gat ccc gat aac cga cgc
2083 Gly Thr Glu Phe Leu Glu Asp Ser Leu Val Asp Pro Asp Asn Arg Arg
650 655 660

ttt gtt gat tac acc gcc aga gaa caa gtc ctg gag cgc ctg caa acc
2131 Phe Val Asp Tyr Thr Ala Arg Glu Gln Val Leu Glu Arg Leu Gln Thr
665 670 675

tgg gct tgg acg cag gtt aat tcg gta gaa gac ttg gtg gat aac gcc
2179 Trp Ala Trp Thr Gln Val Asn Ser Val Glu Asp Leu Val Asp Asn Ala
680 685 690

gac atc gcc aaa atg gcc gtg gtc cat aaa tcc ctc gag ttg cgt gct
2227 Asp Ile Ala Lys Met Ala Val Val His Lys Ser Leu Glu Leu Arg Ala
695 700 705

gaa ttt cgt gca agc ttt gtt ggt gga gat cat cag gca gta ttt ggc
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 Glu Phe Arg Ala Ser Phe Val Gly Gly Asp His Gln Ala Val Phe Gly
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 2323
 Glu Gly Arg Ala Glu Ser His Ile Met Gly Ile Ala Arg Gly Thr Asp
 730 735 740

 cga aac cac ctc aac atc att gct ctt gct acc cgt cga cca ctg atc
 2371
 Arg Asn His Leu Asn Ile Ile Ala Leu Ala Thr Arg Arg Pro Leu Ile
 745 750 755

 ttg gaa gac cgt ggc gga tgg tat gac acc acc gtc acg ctt cct ggt
 2419
 Leu Glu Asp Arg Gly Gly Trp Tyr Asp Thr Thr Val Thr Leu Pro Gly
 760 765 770

 gga caa tgg gaa gac agg ctc acc ggg caa cgcc ttc agt ggt gtt gtc
 2467
 Gly Gln Trp Glu Asp Arg Leu Thr Gly Gln Arg Phe Ser Gly Val Val
 775 780 785

 cca gcc acc gat ttg ttc tca cat cta ccc gta tct ttg ttg gtt tta
 2515
 Pro Ala Thr Asp Leu Phe Ser His Leu Pro Val Ser Leu Leu Val Leu
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 Val Pro Asp Ser Glu Phe
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 <213> Corynebacterium glutamicum

<400> 1142
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 Gln Leu Pro Tyr Leu Lys Lys Leu Gly Ile Ser His Leu Tyr Leu Ser
 35 40 45

 Pro Ile Phe Thr Ala Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile
 50 55 60

 Asp Pro Thr Thr Ile Asn Glu Glu Leu Gly Gly Met Glu Gly Leu Arg
 65 70 75 80

 Asp Leu Ala Ala Ala Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp
 85 90 95

 Ile Val Pro Asn His Leu Gly Val Ala Val Pro His Leu Asn Pro Trp

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Trp Trp Asp Val Leu Lys Asn Gly Lys Asp Ser Ala Phe Glu Phe Tyr		
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Phe Asp Ile Asp Trp His Glu Asp Asn Gly Ser Gly Gly Lys Leu Gly		
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Met Pro Ile Leu Gly Ala Glu Gly Asp Glu Asp Lys Leu Glu Phe Ala		
145	150	155
Glu Leu Asp Gly Glu Lys Val Leu Lys Tyr Phe Asp His Leu Phe Pro		
165	170	175
Ile Ala Pro Gly Thr Glu Glu Gly Thr Pro Gln Glu Val Tyr Lys Arg		
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Gln His Tyr Arg Leu Gln Phe Trp Arg Asp Gly Val Ile Asn Phe Arg		
195	200	205
Arg Phe Phe Ser Val Asn Thr Leu Ala Gly Ile Arg Gln Glu Asp Pro		
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Leu Val Phe Glu His Thr His Arg Leu Leu Arg Glu Leu Val Ala Glu		
225	230	235
Asp Leu Ile Asp Gly Val Arg Val Asp His Pro Asp Gly Leu Ser Asp		
245	250	255
Pro Phe Gly Tyr Leu His Arg Leu Arg Asp Leu Ile Gly Pro Asp Arg		
260	265	270
Trp Leu Ile Ile Glu Lys Ile Leu Ser Val Asp Glu Pro Leu Asp Pro		
275	280	285
Arg Leu Ala Val Asp Gly Thr Thr Gly Tyr Asp Ala Leu Arg Glu Leu		
290	295	300
Asp Gly Val Phe Ile Ser Arg Glu Ser Glu Asp Lys Phe Ser Met Leu		
305	310	315
Ala Leu Thr His Ser Gly Ser Thr Trp Asp Glu Arg Ala Leu Lys Ser		
325	330	335
Thr Glu Glu Ser Leu Lys Arg Val Val Ala Gln Gln Glu Leu Ala Ala		
340	345	350
Glu Ile Leu Arg Leu Ala Arg Ala Met Arg Arg Asp Asn Phe Ser Thr		
355	360	365
Ala Gly Thr Asn Val Thr Glu Asp Lys Leu Ser Glu Thr Ile Ile Glu		
370	375	380
Leu Val Ala Ala Met Pro Val Tyr Arg Ala Asp Tyr Ile Ser Leu Ser		
385	390	395
Arg Thr Thr Ala Thr Val Ile Ala Glu Met Ser Lys Arg Phe Pro Ser		
405	410	415
Arg Arg Asp Ala Leu Asp Leu Ile Ala Ala Ala Leu Leu Gly Asn Gly		
420	425	430

Glu Ala Lys Ile Arg Phe Ala Gln Val Cys Gly Ala Val Met Ala Lys
435 440 445

Gly Val Glu Asp Thr Thr Phe Tyr Arg Ala Ser Arg Leu Val Ala Leu
450 455 460

Gln Glu Val Gly Gly Ala Pro Gly Arg Phe Gly Val Ser Ala Ala Glu
465 470 475 480

Phe His Leu Leu Gln Glu Glu Arg Ser Leu Leu Trp Pro Arg Thr Met
485 490 495

Thr Thr Leu Ser Thr His Asp Thr Lys Arg Gly Glu Asp Thr Arg Ala
500 505 510

Arg Ile Ile Ser Leu Ser Glu Val Pro Asp Met Tyr Ser Glu Leu Val
515 520 525

Asn Arg Val Phe Ala Val Leu Pro Ala Pro Asp Gly Ala Thr Gly Ser
530 535 540

Phe Leu Leu Gln Asn Leu Leu Gly Val Trp Pro Ala Asp Gly Val Ile
545 550 555 560

Thr Asp Ala Leu Arg Asp Arg Phe Arg Glu Tyr Ala Leu Lys Ala Ile
565 570 575

Arg Glu Ala Ser Thr Lys Thr Trp Val Asp Pro Asn Glu Ser Phe
580 585 590

Glu Ala Ala Val Cys Asp Trp Val Glu Ala Leu Phe Asp Gly Pro Ser
595 600 605

Thr Ser Leu Ile Thr Glu Phe Val Ser His Ile Asn Arg Gly Ser Val
610 615 620

Gln Ile Ser Leu Gly Arg Lys Leu Leu Gln Met Val Gly Ala Gly Ile
625 630 635 640

Pro Asp Thr Tyr Gln Gly Thr Glu Phe Leu Glu Asp Ser Leu Val Asp
645 650 655

Pro Asp Asn Arg Arg Phe Val Asp Tyr Thr Ala Arg Glu Gln Val Leu
660 665 670

Glu Arg Leu Gln Thr Trp Ala Trp Thr Gln Val Asn Ser Val Glu Asp
675 680 685

Leu Val Asp Asn Ala Asp Ile Ala Lys Met Ala Val Val His Lys Ser
690 695 700

Leu Glu Leu Arg Ala Glu Phe Arg Ala Ser Phe Val Gly Gly Asp His
705 710 715 720

Gln Ala Val Phe Gly Glu Gly Arg Ala Glu Ser His Ile Met Gly Ile
725 730 735

Ala Arg Gly Thr Asp Arg Asn His Leu Asn Ile Ile Ala Leu Ala Thr
740 745 750

Arg Arg Pro Leu Ile Leu Glu Asp Arg Gly Gly Trp Tyr Asp Thr Thr
 755 760 765

Val Thr Leu Pro Gly Gly Gln Trp Glu Asp Arg Leu Thr Gly Gln Arg
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Ser Leu Leu Val Leu Val Pro Asp Ser Glu Phe
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<213> Corynebacterium glutamicum

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<223> FRXA01239

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 Met Ala Arg Pro Ile
 1 5

tcc gca acg tac agg ctt caa atg cga gga cct caa gca gat agc gcc 163
 Ser Ala Thr Tyr Arg Leu Gln Met Arg Gly Pro Gln Ala Asp Ser Ala
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ggg cgt tca ttt ggt ttt gcg cag gcc aaa gcc cag ctt ccc tat ctg 211
 Gly Arg Ser Phe Gly Phe Ala Gln Ala Lys Ala Gln Leu Pro Tyr Leu
 25 30 35

aag aag cta ggc atc agc cac ctg tac ctc tcc cct att ttt acg gcc 259
 Lys Lys Leu Gly Ile Ser His Leu Tyr Leu Ser Pro Ile Phe Thr Ala
 40 45 50

atg cca gat tcc aat cat ggc tac gat gtc att gat ccc acc acc atc 307
 Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile Asp Pro Thr Thr Ile
 55 60 65

aat gaa gag ctc ggt ggc atg gag ggt ctt cga gat ctt gcc gca gct 355
 Asn Glu Glu Leu Gly Met Glu Gly Leu Arg Asp Leu Ala Ala Ala
 70 75 80 85

aca cac gag ttg ggc atg ggc atc atc att gat att gtt ccc aac cat 403
 Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp Ile Val Pro Asn His
 90 95 100

tta ggt gtt gcc gtt cca cat ttg aat cct tgg tgg tgg gat gtt cta 451
 Leu Gly Val Ala Val Pro His Leu Asn Pro Trp Trp Trp Asp Val Leu
 105 110 115

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 Lys Asn Gly Lys Asp Ser Ala Phe Glu Phe Tyr Phe Asp Ile Asp Trp
 120 125 130

cac gaa gac aac ggt tct ggt ggc aag ctg ggc atg ccg att ctg ggt 547
 His Glu Asp Asn Gly Ser Gly Gly Lys Leu Gly Met Pro Ile Leu Gly
 135 140 145

gct gaa ggc gat gaa gac aag ctg gaa ttc gcg gag ctt gat gga gag 595
 Ala Glu Gly Asp Glu Asp Lys Leu Glu Phe Ala Glu Leu Asp Gly Glu
 150 155 160 165

aaa gtg ctc aaa tat ttt gac cac ctc ttc cca atc gcg cct ggt acc 643
 Lys Val Leu Lys Tyr Phe Asp His Leu Phe Pro Ile Ala Pro Gly Thr
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cag ttc tgg cgc gat ggc gtg atc aac ttc cgt cgc ttc ttt tcc gtg 739
 Gln Phe Trp Arg Asp Gly Val Ile Asn Phe Arg Arg Phe Phe Ser Val
 200 205 210

aat acg ttg gct ggc atc agg caa gaa gat ccc tta gtg ttt gaa cat 787
 Asn Thr Leu Ala Gly Ile Arg Gln Glu Asp Pro Leu Val Phe Glu His
 215 220 225

act cat cgt ctg ctg cgc gaa ttg gtg gcg gaa gac ctc att gac ggc 835
 Thr His Arg Leu Leu Arg Glu Leu Val Ala Glu Asp Leu Ile Asp Gly
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gtg cgc gtc gat cac ccc gac ggg ctt tcc gat cct ttt gga tat ctg 883
 Val Arg Val Asp His Pro Asp Gly Leu Ser Asp Pro Phe Gly Tyr Leu
 250 255 260

cac aga ctc cgc gac ctc att gga cct gac cgc tgg ctg atc atc gaa 931
 His Arg Leu Arg Asp Leu Ile Gly Pro Asp Arg Trp Leu Ile Ile Glu
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 Lys Ile Leu Ser Val Asp Glu Pro Leu Asp Pro Arg Leu Ala Val Asp
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375 380 385

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Val Ile Ala Glu Met Ser Lys Arg Phe Pro Ser Arg Arg Asp Ala Leu
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1411
Asp Leu Ile Ala Ala Leu Leu Gly Asn Gly Glu Ala Lys Ile Arg
425 430 435

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1555
Ala Pro Gly Arg Phe Gly Val Ser Ala Ala Glu Phe His Leu Leu Gln
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Glu Glu Arg Ser Leu Leu Trp Pro Arg Thr Met Thr Thr Leu Ser Thr
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His Asp Thr Lys Arg Gly Glu Asp Thr Arg Ala Arg Ile Ile Ser Leu
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Asp Arg Phe Arg Glu Tyr Ala Leu Lys Ala Ile Arg Glu Ala Ser Thr
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1891
Lys Thr Thr Trp Val Asp Pro Asn Glu Ser Phe Glu Ala Ala Val Cys
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1939
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2227
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695 700 705
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2323
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730 735 740

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 2371
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 Val Pro Asp Ser Glu Phe
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 35 40 45

Pro Ile Phe Thr Ala Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile
 50 55 60

Asp Pro Thr Thr Ile Asn Glu Glu Leu Gly Gly Met Glu Gly Leu Arg
 65 70 75 80

Asp Leu Ala Ala Ala Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp
 85 90 95

Ile Val Pro Asn His Leu Gly Val Ala Val Pro His Leu Asn Pro Trp
 100 105 110

Trp Trp Asp Val Leu Lys Asn Gly Lys Asp Ser Ala Phe Glu Phe Tyr
 115 120 125

Phe Asp Ile Asp Trp His Glu Asp Asn Gly Ser Gly Gly Lys Leu Gly
 130 135 140

Met Pro Ile Leu Gly Ala Glu Gly Asp Glu Asp Lys Leu Glu Phe Ala
 145 150 155 160

Glu Leu Asp Gly Glu Lys Val Leu Lys Tyr Phe Asp His Leu Phe Pro
165 170 175

Ile Ala Pro Gly Thr Glu Glu Gly Thr Pro Gln Glu Val Tyr Lys Arg
180 185 190

Gln His Tyr Arg Leu Gln Phe Trp Arg Asp Gly Val Ile Asn Phe Arg
195 200 205

Arg Phe Phe Ser Val Asn Thr Leu Ala Gly Ile Arg Gln Glu Asp Pro
210 215 220

Leu Val Phe Glu His Thr His Arg Leu Leu Arg Glu Leu Val Ala Glu
225 230 235 240

Asp Leu Ile Asp Gly Val Arg Val Asp His Pro Asp Gly Leu Ser Asp
245 250 255

Pro Phe Gly Tyr Leu His Arg Leu Arg Asp Leu Ile Gly Pro Asp Arg
260 265 270

Trp Leu Ile Ile Glu Lys Ile Leu Ser Val Asp Glu Pro Leu Asp Pro
275 280 285

Arg Leu Ala Val Asp Gly Thr Thr Gly Tyr Asp Ala Leu Arg Glu Leu
290 295 300

Asp Gly Val Phe Ile Ser Arg Glu Ser Glu Asp Lys Phe Ser Met Leu
305 310 315 320

Ala Leu Thr His Ser Gly Ser Thr Trp Asp Glu Arg Ala Leu Lys Ser
325 330 335

Thr Glu Glu Ser Leu Lys Arg Val Val Ala Gln Gln Glu Leu Ala Ala
340 345 350

Glu Ile Leu Arg Leu Ala Arg Ala Met Arg Arg Asp Asn Phe Ser Thr
355 360 365

Ala Gly Thr Asn Val Thr Glu Asp Lys Leu Ser Glu Thr Ile Ile Glu
370 375 380

Leu Val Ala Ala Met Pro Val Tyr Arg Ala Asp Tyr Ile Ser Leu Ser
385 390 395 400

Arg Thr Thr Ala Thr Val Ile Ala Glu Met Ser Lys Arg Phe Pro Ser
405 410 415

Arg Arg Asp Ala Leu Asp Leu Ile Ala Ala Ala Leu Leu Gly Asn Gly
420 425 430

Glu Ala Lys Ile Arg Phe Ala Gln Val Cys Gly Ala Val Met Ala Lys
435 440 445

Gly Val Glu Asp Thr Thr Phe Tyr Arg Ala Ser Arg Leu Val Ala Leu
450 455 460

Gln Glu Val Gly Gly Ala Pro Gly Arg Phe Gly Val Ser Ala Ala Glu
465 470 475 480

Phe His Leu Leu Gln Glu Glu Arg Ser Leu Leu Trp Pro Arg Thr Met
485 490 495

Thr Thr Leu Ser Thr His Asp Thr Lys Arg Gly Glu Asp Thr Arg Ala
500 505 510

Arg Ile Ile Ser Leu Ser Glu Val Pro Asp Met Tyr Ser Glu Leu Val
515 520 525

Asn Arg Val Phe Ala Val Leu Pro Ala Pro Asp Gly Ala Thr Gly Ser
530 535 540

Phe Leu Leu Gln Asn Leu Leu Gly Val Trp Pro Ala Asp Gly Val Ile
545 550 555 560

Thr Asp Ala Leu Arg Asp Arg Phe Arg Glu Tyr Ala Leu Lys Ala Ile
565 570 575

Arg Glu Ala Ser Thr Lys Thr Trp Val Asp Pro Asn Glu Ser Phe
580 585 590

Glu Ala Ala Val Cys Asp Trp Val Glu Ala Leu Phe Asp Gly Pro Ser
595 600 605

Thr Ser Leu Ile Thr Glu Phe Val Ser His Ile Asn Arg Gly Ser Val
610 615 620

Gln Ile Ser Leu Gly Arg Lys Leu Leu Gln Met Val Gly Ala Gly Ile
625 630 635 640

Pro Asp Thr Tyr Gln Gly Thr Glu Phe Leu Glu Asp Ser Leu Val Asp
645 650 655

Pro Asp Asn Arg Arg Phe Val Asp Tyr Thr Ala Arg Glu Gln Val Leu
660 665 670

Glu Arg Leu Gln Thr Trp Asp Trp Thr Gln Val Asn Ser Val Glu Asp
675 680 685

Leu Val Asp Asn Ala Asp Ile Ala Lys Met Ala Val Val His Lys Ser
690 695 700

Leu Glu Leu Arg Ala Glu Phe Arg Ala Ser Phe Val Gly Gly Asp His
705 710 715 720

Gln Ala Val Phe Gly Glu Gly Arg Ala Glu Ser His Ile Met Gly Ile
725 730 735

Ala Arg Gly Thr Asp Arg Asn His Leu Asn Ile Ile Ala Leu Ala Thr
740 745 750

Arg Arg Pro Leu Ile Leu Glu Asp Arg Gly Gly Trp Tyr Asp Thr Thr
755 760 765

Val Thr Leu Pro Gly Gly Gln Trp Glu Asp Arg Leu Thr Gly Gln Arg
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805

810

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<213> Corynebacterium glutamicum

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<222> (101)..(1930)
<223> RXA02645

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acc ggc ctg agg gag ttg gta ttg cgt gag atg tgc cat agc atc tca 163
Thr Gly Leu Arg Glu Leu Val Leu Arg Glu Met Cys His Ser Ile Ser
10 15 20
cat ctt agc tcg cca acc ggc agc att ttc act agc ctg gtg gcc atg 211
His Leu Ser Ser Pro Thr Gly Ser Ile Phe Thr Ser Leu Val Ala Met
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Leu Thr Ser Gln Ser Phe Ser Val Trp Ala Pro Leu Pro His Asp Val
40 45 50
cat ctg atc ctc aac ggc gaa acc ctc ccc atg cac aaa acg gag ggc 307
His Leu Ile Leu Asn Gly Glu Thr Leu Pro Met His Lys Thr Glu Gly
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Ser Trp Trp Arg Ala Glu Ile Ala Pro Lys Ala Gly Asp Arg Tyr Gly
70 75 80 85
ttt tcg ctt ttc gac ggc tcc tcc tgg tca aaa acc ctc ccc gat ccc 403
Phe Ser Leu Phe Asp Gly Ser Ser Trp Ser Lys Thr Leu Pro Asp Pro
90 95 100
cgc tcc aca tct caa cca gac ggg gtt cat ggt tta agt gaa gtc tcc 451
Arg Ser Thr Ser Gln Pro Asp Gly Val His Gly Leu Ser Glu Val Ser
105 110 115
gat gat tcc tat ctg tgg ggt gac cag cag tgg act ggc cga att ctc 499
Asp Asp Ser Tyr Leu Trp Gly Asp Gln Gln Trp Thr Gly Arg Ile Leu
120 125 130
cct ggc tcg gtg tta tat gag ctg cat gtg ggc acc ttt agt gaa gat 547
Pro Gly Ser Val Leu Tyr Glu Leu His Val Gly Thr Phe Ser Glu Asp
135 140 145
gga acg ttt gag gga gtc gtc gac aag ctt cct tat ctg cgc gac ctc 595
Gly Thr Phe Glu Gly Val Val Asp Lys Leu Pro Tyr Leu Arg Asp Leu
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ggc gtg acc gcc atc gaa ctt tta ccc gtg cag ccc ttt ggc ggc aac 643

Gly Val Thr Ala Ile Glu Leu Leu Pro Val Gln Pro Phe Gly Gly Asn
170 175 180

cgc aat tgg ggc tac gac ggg gtg ctg tgg cac gcc gtc cat gca ggc 691
Arg Asn Trp Gly Tyr Asp Gly Val Leu Trp His Ala Val His Ala Gly
185 190 195

tac ggc ggt ccg gcg ggc ttg aaa aag ctt atc gac gcc tcc cac cag 739
Tyr Gly Gly Pro Ala Gly Leu Lys Lys Leu Ile Asp Ala Ser His Gln
200 205 210

gcc ggc atc gcc gtc tac tta gac gtc gtg tac aac cac ttc ggc ccc 787
Ala Gly Ile Ala Val Tyr Leu Asp Val Val Tyr Asn His Phe Gly Pro
215 220 225

gac ggc aac tac aac ggg caa ttt ggc ccc tac acc tct ggc ggc agc 835
Asp Gly Asn Tyr Asn Gly Gln Phe Gly Pro Tyr Thr Ser Gly Gly Ser
230 235 240 245

acc ggc tgg ggc gac gtg gtc aac atc aac ggc cat gat tca gat gaa 883
Thr Gly Trp Gly Asp Val Val Asn Ile Asn Gly His Asp Ser Asp Glu
250 255 260

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Val Arg Asn Tyr Ile Leu Asp Ala Ala Arg Gln Trp Phe Glu Asp Phe
265 270 275

cac gtt gat ggg ctc cgc ctc gat gcg gtg cat tct ctc gat gat cgc 979
His Val Asp Gly Leu Arg Leu Asp Ala Val His Ser Leu Asp Asp Arg
280 285 290

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1027
Gly Ala Tyr Ser Leu Leu Ala Gln Leu Thr Met Val Ala Glu Asp Val
295 300 305

tcc gca caa aca ggc atc cca cgc tca ttg att gca gaa tct gaa ctc
1075
Ser Ala Gln Thr Gly Ile Pro Arg Ser Leu Ile Ala Glu Ser Glu Leu
310 315 320 325

aat gac ccc aag ttc gtt acc tcc cgc gag gcc ggc ggt ttt ggc ctg
1123
Asn Asp Pro Lys Phe Val Thr Ser Arg Glu Ala Gly Gly Phe Gly Leu
330 335 340

gat gca cag tgg gtt gac gat atc cac cac gcc ctc cat gcc ctc gtt
1171
Asp Ala Gln Trp Val Asp Asp Ile His His Ala Leu His Ala Leu Val
345 350 355

tct ggc gaa cgc aat ggt tat tac agc gat ttc gga tct gtc gac aca
1219
Ser Gly Glu Arg Asn Gly Tyr Tyr Ser Asp Phe Gly Ser Val Asp Thr
360 365 370

tta gcc aaa acc ctg cgt gaa gta ttt gaa cac acc gga aac tac tcc
1267
Leu Ala Lys Thr Leu Arg Glu Val Phe Glu His Thr Gly Asn Tyr Ser
375 380 385

gag ctg att tac agc ttc act tcc ccc acc gtc acc gac acc tcc aca
1891
Glu Leu Ile Tyr Ser Phe Thr Ser Pro Thr Val Thr Asp Thr Ser Thr
585 590 595

acc ctt cag ccg tgg ggc ttt gcg atc ctg acc cga aac tagaaaaagg
1940
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600 605 610

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1953

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<400> 1146
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Cys His Ser Ile Ser His Leu Ser Ser Pro Thr Gly Ser Ile Phe Thr
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35 40 45

Leu Pro His Asp Val His Leu Ile Leu Asn Gly Glu Thr Leu Pro Met
50 55 60

His Lys Thr Glu Gly Ser Trp Trp Arg Ala Glu Ile Ala Pro Lys Ala
65 70 75 80

Gly Asp Arg Tyr Gly Phe Ser Leu Phe Asp Gly Ser Ser Trp Ser Lys
85 90 95

Thr Leu Pro Asp Pro Arg Ser Thr Ser Gln Pro Asp Gly Val His Gly
100 105 110

Leu Ser Glu Val Ser Asp Asp Ser Tyr Leu Trp Gly Asp Gln Gln Trp
115 120 125

Thr Gly Arg Ile Leu Pro Gly Ser Val Leu Tyr Glu Leu His Val Gly
130 135 140

Thr Phe Ser Glu Asp Gly Thr Phe Glu Gly Val Val Asp Lys Leu Pro
145 150 155 160

Tyr Leu Arg Asp Leu Gly Val Thr Ala Ile Glu Leu Leu Pro Val Gln
165 170 175

Pro Phe Gly Gly Asn Arg Asn Trp Gly Tyr Asp Gly Val Leu Trp His
180 185 190

Ala Val His Ala Gly Tyr Gly Gly Pro Ala Gly Leu Lys Lys Leu Ile
195 200 205

Asp Ala Ser His Gln Ala Gly Ile Ala Val Tyr Leu Asp Val Val Tyr
210 215 220

acg tac cgc gga cgc aac cac ggc cgc cct gtg cac ccc gat atc acc
1315
Thr Tyr Arg Gly Arg Asn His Gly Arg Pro Val His Pro Asp Ile Thr
390 395 400 405

cct gcc tcg cgc ttt gtc acc tac acc acc acc cat gat cag acc ggc
1363
Pro Ala Ser Arg Phe Val Thr Tyr Thr Thr His Asp Gln Thr Gly
410 415 420

aac cgc gca atc ggc gac cgt cct tcc acg act ctc acc ccg gaa cag
1411
Asn Arg Ala Ile Gly Asp Arg Pro Ser Thr Thr Leu Thr Pro Glu Gln
425 430 435

cag gtg ttg aag gca gcc att atc tac agc tcg ccg tat acc ccg atg
1459
Gln Val Leu Lys Ala Ala Ile Ile Tyr Ser Ser Pro Tyr Thr Pro Met
440 445 450

ttg ttt atg ggt gaa gaa ttc gga gcc acc acc cca ttc gcc ttc ttt
1507
Leu Phe Met Gly Glu Glu Phe Gly Ala Thr Thr Pro Phe Ala Phe Phe
455 460 465

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1555
Cys Ser His Thr Asp Pro Glu Leu Asn Arg Leu Thr Ser Glu Gly Arg
470 475 480 485

aaa cgg gaa ttc gca cgc ctt ggc tgg aac gcc gac gac atc ccc tcc
1603
Lys Arg Glu Phe Ala Arg Leu Gly Trp Asn Ala Asp Asp Ile Pro Ser
490 495 500

ccc gag ctg gaa tcc acc ttc acc tcc tcc aaa ctc gat tgg gag ttc
1651
Pro Glu Leu Glu Ser Thr Phe Thr Ser Ser Lys Leu Asp Trp Glu Phe
505 510 515

act gcg gag cag cgc cgc atc aac gac gct tac aag cag ctg ttg cac
1699
Thr Ala Glu Gln Arg Arg Ile Asn Asp Ala Tyr Lys Gln Leu Leu His
520 525 530

ctg cgg cac acc ttg ggc ttc tcc caa cca aac ttg ctc aca ctc gag
1747
Leu Arg His Thr Leu Gly Phe Ser Gln Pro Asn Leu Leu Thr Leu Glu
535 540 545

gtt gag cac ggc gag aac tgg cta tcg atg gcc aat ggt cgc ggc cga
1795
Val Glu His Gly Glu Asn Trp Leu Ser Met Ala Asn Gly Arg Gly Arg
550 555 560 565

att ctg gcg aat ttc tcc gac gac acc atc acc gtc ccg ctt ggc ggc
1843
Ile Leu Ala Asn Phe Ser Asp Asp Thr Ile Thr Val Pro Leu Gly Gly
570 575 580

Asn His Phe Gly Pro Asp Gly Asn Tyr Asn Gly Gln Phe Gly Pro Tyr
225 230 235 240

Thr Ser Gly Gly Ser Thr Gly Trp Gly Asp Val Val Asn Ile Asn Gly
245 250 255

His Asp Ser Asp Glu Val Arg Asn Tyr Ile Leu Asp Ala Ala Arg Gln
260 265 270

Trp Phe Glu Asp Phe His Val Asp Gly Leu Arg Leu Asp Ala Val His
275 280 285

Ser Leu Asp Asp Arg Gly Ala Tyr Ser Leu Leu Ala Gln Leu Thr Met
290 295 300

Val Ala Glu Asp Val Ser Ala Gln Thr Gly Ile Pro Arg Ser Leu Ile
305 310 315 320

Ala Glu Ser Glu Leu Asn Asp Pro Lys Phe Val Thr Ser Arg Glu Ala
325 330 335

Gly Gly Phe Gly Leu Asp Ala Gln Trp Val Asp Asp Ile His His Ala
340 345 350

Leu His Ala Leu Val Ser Gly Glu Arg Asn Gly Tyr Tyr Ser Asp Phe
355 360 365

Gly Ser Val Asp Thr Leu Ala Lys Thr Leu Arg Glu Val Phe Glu His
370 375 380

Thr Gly Asn Tyr Ser Thr Tyr Arg Gly Arg Asn His Gly Arg Pro Val
385 390 395 400

His Pro Asp Ile Thr Pro Ala Ser Arg Phe Val Thr Tyr Thr Thr Thr
405 410 415

His Asp Gln Thr Gly Asn Arg Ala Ile Gly Asp Arg Pro Ser Thr Thr
420 425 430

Leu Thr Pro Glu Gln Gln Val Leu Lys Ala Ala Ile Ile Tyr Ser Ser
435 440 445

Pro Tyr Thr Pro Met Leu Phe Met Gly Glu Glu Phe Gly Ala Thr Thr
450 455 460

Pro Phe Ala Phe Phe Cys Ser His Thr Asp Pro Glu Leu Asn Arg Leu
465 470 475 480

Thr Ser Glu Gly Arg Lys Arg Glu Phe Ala Arg Leu Gly Trp Asn Ala
485 490 495

Asp Asp Ile Pro Ser Pro Glu Leu Glu Ser Thr Phe Thr Ser Ser Lys
500 505 510

Leu Asp Trp Glu Phe Thr Ala Glu Gln Arg Arg Ile Asn Asp Ala Tyr
515 520 525

Lys Gln Leu Leu His Leu Arg His Thr Leu Gly Phe Ser Gln Pro Asn
530 535 540

Leu Leu Thr Leu Glu Val Glu His Gly Glu Asn Trp Leu Ser Met Ala
545 550 555 560

Asn Gly Arg Gly Arg Ile Leu Ala Asn Phe Ser Asp Asp Thr Ile Thr
565 570 575

Val Pro Leu Gly Gly Glu Leu Ile Tyr Ser Phe Thr Ser Pro Thr Val
580 585 590

Thr Asp Thr Ser Thr Thr Leu Gln Pro Trp Gly Phe Ala Ile Leu Thr
595 600 605

Arg Asn
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<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(832)

<223> RXN02355

<400> 1147

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Met Ser Ser Ile Ser
1 5

cgc aag acc ggc gcg tca ctt gca gcc acc aca ctg ttg gca gcg atc 163
Arg Lys Thr Gly Ala Ser Leu Ala Ala Thr Thr Leu Leu Ala Ala Ile
10 15 20

gca ctg gcc ggt tgt agt tca gac tca agc tcc gac tcc aca gat tcc 211
Ala Leu Ala Gly Cys Ser Ser Asp Ser Ser Ser Asp Ser Thr Asp Ser
25 30 35

acc gct agc gaa ggc gca gac agc cgc ggc ccc atc acc ttt gcg atg 259
Thr Ala Ser Glu Gly Ala Asp Ser Arg Gly Pro Ile Thr Phe Ala Met
40 45 50

ggc aaa aac gac acc gac aaa gtc att ccg atc atc gac cgc tgg aac 307
Gly Lys Asn Asp Thr Asp Lys Val Ile Pro Ile Ile Asp Arg Trp Asn
55 60 65

gaa gcc cac ccc gat gag cag gta acg ctc aac gaa ctc gcc ggt gaa 355
Glu Ala His Pro Asp Glu Gln Val Thr Leu Asn Glu Leu Ala Gly Glu
70 75 80 85

gcc gac gcg cag cgc gaa acc ctc gtg caa tcc ctg cag gcc ggc aac 403
Ala Asp Ala Gln Arg Glu Thr Leu Val Gln Ser Leu Gln Ala Gly Asn
90 95 100

tct gac tac gac gtc atg gcg ctc gac gtc atc tgg acc gca gac ttc 451
Ser Asp Tyr Asp Val Met Ala Leu Asp Val Ile Trp Thr Ala Asp Phe
105 110 115

gcg gca aac caa tgg ctc gca cca ctt gaa ggc gac ctc gag gta gac 499
 Ala Ala Asn Gln Trp Leu Ala Pro Leu Glu Gly Asp Leu Glu Val Asp
 120 125 130

acc tcc gga ctg ctg caa tcc acc gtg gat tcc gca acc tac aac ggc 547
 Thr Ser Gly Leu Leu Gln Ser Thr Val Asp Ser Ala Thr Tyr Asn Gly
 135 140 145

acc ctc tac gca ctg cca cag aac acc aac ggc cag cta ctg ttc cgc 595
 Thr Leu Tyr Ala Leu Pro Gln Asn Thr Asn Gly Gln Leu Leu Phe Arg
 150 155 160 165

aac acc gaa atc atc cca gaa gca cca gca aac tgg gct gac ctc gtg 643
 Asn Thr Glu Ile Ile Pro Glu Ala Pro Ala Asn Trp Ala Asp Leu Val
 170 175 180

gaa tcc tgc acg ctt gct gaa gaa gca ggc gtt gat tgc ctg acc act 691
 Glu Ser Cys Thr Leu Ala Glu Glu Ala Gly Val Asp Cys Leu Thr Thr
 185 190 195

cag ctc aag cag tac gaa ggc ctt tca gtg aac acc atc ggc ttc atc 739
 Gln Leu Lys Gln Tyr Glu Gly Leu Ser Val Asn Thr Ile Gly Phe Ile
 200 205 210

gaa ggt tgg gga ggc agc gtc cta gac gat gac ggc aaa cgt cac cgt 787
 Glu Gly Trp Gly Gly Ser Val Leu Asp Asp Asp Gly Lys Arg His Arg
 215 220 225

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<211> 244

<212> PRT

<213> Corynebacterium glutamicum

<400> 1148

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 35 40 45

Ile Thr Phe Ala Met Gly Lys Asn Asp Thr Asp Lys Val Ile Pro Ile
 50 55 60

Ile Asp Arg Trp Asn Glu Ala His Pro Asp Glu Gln Val Thr Leu Asn
 65 70 75 80

Glu Leu Ala Gly Glu Ala Asp Ala Gln Arg Glu Thr Leu Val Gln Ser
 85 90 95

Leu Gln Ala Gly Asn Ser Asp Tyr Asp Val Met Ala Leu Asp Val Ile
 100 105 110

Trp Thr Ala Asp Phe Ala Ala Asn Gln Trp Leu Ala Pro Leu Glu Gly

115	120	125
Asp Leu Glu Val Asp Thr Ser Gly Leu Leu Gln Ser Thr Val Asp Ser		
130	135	140
Ala Thr Tyr Asn Gly Thr Leu Tyr Ala Leu Pro Gln Asn Thr Asn Gly		
145	150	155
Gln Leu Leu Phe Arg Asn Thr Glu Ile Ile Pro Glu Ala Pro Ala Asn		
165	170	175
Trp Ala Asp Leu Val Glu Ser Cys Thr Leu Ala Glu Glu Ala Gly Val		
180	185	190
Asp Cys Leu Thr Thr Gln Leu Lys Gln Tyr Glu Gly Leu Ser Val Asn		
195	200	205
Thr Ile Gly Phe Ile Glu Gly Trp Gly Gly Ser Val Leu Asp Asp Asp		
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Leu Val Asp Gly		

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Met Asn Arg Ala Arg
1 5
atc gcg acc ata ggc gtt ctt ccg ctt gct tta ctg ctg gcg tcc tgt 163
Ile Ala Thr Ile Gly Val Leu Pro Leu Ala Leu Leu Ala Ser Cys
10 15 20
ggt tca gac acc gtg gaa atg aca gat tcc acc tgg ttg gtg acc aat 211
Gly Ser Asp Thr Val Glu Met Thr Asp Ser Thr Trp Leu Val Thr Asn
25 30 35
att tac acc gat cca gat gag tcg aat tcg atc agt aat ctt gtc att 259
Ile Tyr Thr Asp Pro Asp Glu Ser Asn Ser Ile Ser Asn Leu Val Ile
40 45 50
tcc cag ccc agc tta gat ttt ggc aat tct tcc ctg tct ggt ttc act 307
Ser Gln Pro Ser Leu Asp Phe Gly Asn Ser Ser Leu Ser Gly Phe Thr
55 60 65
ggc tgt gtg cct ttt acg ggg cgt gcg gaa ttc ttc caa aat ggt gag 355

Gly	Cys	Val	Pro	Phe	Thr	Gly	Arg	Ala	Glu	Phe	Phe	Gln	Asn	Gly	Glu	
70						75			80			85				
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Gln	Ser	Ser	Val	Leu	Asp	Ala	Asp	Tyr	Val	Thr	Leu	Ser	Ser	Leu	Asp	
						90				95					100	
ttc	gat	aaa	ctt	ccc	gat	gat	tgc	caa	gga	caa	gaa	ctc	aaa	gtt	cat	451
Phe	Asp	Lys	Leu	Pro	Asp	Asp	Cys	Gln	Gly	Gln	Glu	Leu	Lys	Val	His	
						105			110			115				
aac	gag	ctg	gtt	gat	ctt	ctg	cct	ggt	tct	ttt	gaa	atc	tcc	agg	act	499
Asn	Glu	Leu	Val	Asp	Leu	Leu	Pro	Gly	Ser	Phe	Glu	Ile	Ser	Arg	Thr	
						120			125			130				
tct	ggt	tca	gaa	atc	ttg	ctg	act	agc	gat	gtc	gat	gaa	ctc	gat	cgg	547
Ser	Gly	Ser	Glu	Ile	Leu	Leu	Thr	Ser	Asp	Val	Asp	Glu	Leu	Asp	Arg	
						135			140			145				
cca	gca	atc	cgc	ttg	gtg	tcc	tgg	atc	gcg	ccg	aca	tct	taaggtgccaa		596	
Pro	Ala	Ile	Arg	Leu	Val	Ser	Trp	Ile	Ala	Pro	Thr	Ser				
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					20				25			30				
Trp	Leu	Val	Thr	Asn	Ile	Tyr	Thr	Asp	Pro	Asp	Glu	Ser	Asn	Ser	Ile	
					35			40			45					
Ser	Asn	Leu	Val	Ile	Ser	Gln	Pro	Ser	Leu	Asp	Phe	Gly	Asn	Ser	Ser	
					50			55			60					
Leu	Ser	Gly	Phe	Thr	Gly	Cys	Val	Pro	Phe	Thr	Gly	Arg	Ala	Glu	Phe	
					65			70			75			80		
Phe	Gln	Asn	Gly	Glu	Gln	Ser	Ser	Val	Leu	Asp	Ala	Asp	Tyr	Val	Thr	
					85				90			95				
Leu	Ser	Ser	Leu	Asp	Phe	Asp	Lys	Leu	Pro	Asp	Asp	Cys	Gln	Gly	Gln	
					100			105			110					
Glu	Leu	Lys	Val	His	Asn	Glu	Leu	Val	Asp	Leu	Leu	Pro	Gly	Ser	Phe	
					115			120			125					
Glu	Ile	Ser	Arg	Thr	Ser	Gly	Ser	Glu	Ile	Leu	Leu	Thr	Ser	Asp	Val	
					130			135			140					
Asp	Glu	Leu	Asp	Arg	Pro	Ala	Ile	Arg	Leu	Val	Ser	Trp	Ile	Ala	Pro	
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Thr Ser

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<211> 1590

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1567)

<223> RXS00349

<400> 1151

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Met Leu Ser Phe Ala
1 5acc ctt cgt ggc cgc att tca aca gtt gac gct gca aaa gcc gca cct 163
Thr Leu Arg Gly Arg Ile Ser Thr Val Asp Ala Ala Lys Ala Ala Pro
10 15 20ccg cca tcg cca cta gcc ccg att gat ctc act gac cat agt caa gtg 211
Pro Pro Ser Pro Leu Ala Pro Ile Asp Leu Thr Asp His Ser Gln Val
25 30 35gcc ggt gtg atg aat ttg gct gcg aga att ggc gat att ttg ctt tct 259
Ala Gly Val Met Asn Leu Ala Ala Arg Ile Gly Asp Ile Leu Leu Ser
40 45 50tca ggt acg tca aat agt gac acc aag gta caa gtt cga gca gtg acc 307
Ser Gly Thr Ser Asn Ser Asp Thr Lys Val Gln Val Arg Ala Val Thr
55 60 65tct gcg tac ggt ttg tac tac acg cac gtg gat atc acg ttg aat acg 355
Ser Ala Tyr Gly Leu Tyr Tyr His Val Asp Ile Thr Leu Asn Thr
70 75 80 85atc acc atc ttc acc aac atc ggt gtg gag agg aag atg ccg gtc aac 403
Ile Thr Ile Phe Thr Asn Ile Gly Val Glu Arg Lys Met Pro Val Asn
90 95 100gtg ttt cat gtt gta ggc aag ttg gac acc aac ttc tcc aaa ctg tct 451
Val Phe His Val Val Gly Lys Leu Asp Thr Asn Phe Ser Lys Leu Ser
105 110 115gag gtt gac cgt ttg atc cgt tcc att cag gct ggt gcg acc ccg cct 499
Glu Val Asp Arg Leu Ile Arg Ser Ile Gln Ala Gly Ala Thr Pro Pro
120 125 130gag gtt gcc gag aaa atc ctg gac gag ttg gag caa tcc cct gcg tct 547
Glu Val Ala Glu Lys Ile Leu Asp Glu Leu Glu Gln Ser Pro Ala Ser
135 140 145tat ggt ttc cct gtt gcg ttg ctt ggc tgg gca atg atg ggt ggt gct 595
Tyr Gly Phe Pro Val Ala Leu Leu Gly Trp Ala Met Met Gly Gly Ala
150 155 160 165

gtt gct gtg ctg ttg ggt ggt gga tgg cag gtt tcc cta att gct ttt 643
 Val Ala Val Leu Leu Gly Gly Trp Gln Val Ser Leu Ile Ala Phe
 170 175 180

 att acc gcg ttc acg atc att gcc acg acg tca ttt ttg gga aag aag 691
 Ile Thr Ala Phe Thr Ile Ile Ala Thr Thr Ser Phe Leu Gly Lys Lys
 185 190 195

 ggt ttg cct act ttc ttc caa aat gtt gtt ggt ggt ttt att gcc acg 739
 Gly Leu Pro Thr Phe Phe Gln Asn Val Val Gly Gly Phe Ile Ala Thr
 200 205 210

 ctg cct gca tcg att gct tat tct ttg gcg ttg caa ttt ggt ctt gag 787
 Leu Pro Ala Ser Ile Ala Tyr Ser Leu Ala Leu Gln Phe Gly Leu Glu
 215 220 225

 atc aaa ccg agc cag atc atc gca tct gga att gtt gtg ctg ttg gca 835
 Ile Lys Pro Ser Gln Ile Ile Ala Ser Gly Ile Val Val Leu Leu Ala
 230 235 240 245

 ggt ttg aca ctc gtg caa tct ctg cag gac ggc atc acg ggc gct ccg 883
 Gly Leu Thr Leu Val Gln Ser Leu Gln Asp Gly Ile Thr Gly Ala Pro
 250 255 260

 gtg aca gca agt gca cga ttt ttc gaa aca ctc ctg ttt acc ggc ggc 931
 Val Thr Ala Ser Ala Arg Phe Phe Glu Thr Leu Leu Phe Thr Gly Gly
 265 270 275

 att gtt gct ggc gtg ggt ttg ggc att cag ctt tct gaa atc ttg cat 979
 Ile Val Ala Gly Val Gly Leu Gly Ile Gln Leu Ser Glu Ile Leu His
 280 285 290

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 Val Met Leu Pro Ala Met Glu Ser Ala Ala Ala Pro Asn Tyr Ser Ser
 295 300 305

 aca ttc gcc cgc att atc gct ggt ggc gtc acc gca gcg gcc ttc gca
 1075
 Thr Phe Ala Arg Ile Ile Ala Gly Gly Val Thr Ala Ala Ala Phe Ala
 310 315 320 325

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 1123
 Val Gly Cys Tyr Ala Glu Trp Ser Ser Val Ile Ile Ala Gly Leu Thr
 330 335 340

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 1171
 Ala Leu Met Gly Ser Ala Phe Tyr Tyr Leu Phe Val Val Tyr Leu Gly
 345 350 355

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 1219
 Pro Val Ser Ala Ala Ala Ile Ala Ala Thr Ala Val Gly Phe Thr Gly
 360 365 370

 ggt ttg ctt gcc cgt cga ttc ttg att cca ccg ttg att gtg gcg att
 1267
 Gly Leu Leu Ala Arg Arg Phe Leu Ile Pro Pro Leu Ile Val Ala Ile

375	380	385													
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Ala	Gly	Ile	Thr	Pro	Met	Leu	Pro	Gly	Leu	Ala	Ile	Tyr	Arg	Gly	Met
390				395				400						405	
tac gcc acc ctg aat gat caa aca ctc atg ggt ttc acc aac att gcg 1363															
Tyr	Ala	Thr	Leu	Asn	Asp	Gln	Thr	Leu	Met	Gly	Phe	Thr	Asn	Ile	Ala
				410				415					420		
gtt gct tta gcc act gct tca tca ctt gcc gct ggc gtg gtt ttg ggt 1411															
Val	Ala	Leu	Ala	Thr	Ala	Ser	Ser	Leu	Ala	Ala	Gly	Val	Val	Leu	Gly
				425				430				435			
gag tgg att gcc cgc agg cta cgt cgt cca cca cgc ttc aac cca tac 1459															
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				440			445				450				
cgt gca ttt acc aag gcg aat gag ttc tcc ttc cag gag gaa gct gag 1507															
Arg	Ala	Phe	Thr	Lys	Ala	Asn	Glu	Phe	Ser	Phe	Gln	Glu	Glu	Ala	Glu
				455			460				465				
cag aat cag cgc cg ^g cag aga aaa cgt cca aag act aat cag aga ttc 1555															
Gln	Asn	Gln	Arg	Arg	Gln	Arg	Lys	Arg	Pro	Lys	Thr	Asn	Gln	Arg	Phe
				470			475			480			485		
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					20				25			30			
Asp	His	Ser	Gln	Val	Ala	Gly	Val	Met	Asn	Leu	Ala	Ala	Arg	Ile	Gly
				35			40					45			
Asp	Ile	Leu	Leu	Ser	Ser	Gly	Thr	Ser	Asn	Ser	Asp	Thr	Lys	Val	Gln
				50			55			60					
Val	Arg	Ala	Val	Thr	Ser	Ala	Tyr	Gly	Leu	Tyr	Tyr	Thr	His	Val	Asp
				65			70			75			80		
Ile	Thr	Leu	Asn	Thr	Ile	Thr	Ile	Phe	Thr	Asn	Ile	Gly	Val	Glu	Arg
					85				90			95			

Lys Met Pro Val Asn Val Phe His Val Val Gly Lys Leu Asp Thr Asn
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 Phe Ser Lys Leu Ser Glu Val Asp Arg Leu Ile Arg Ser Ile Gln Ala
 115 120 125
 Gly Ala Thr Pro Pro Glu Val Ala Glu Lys Ile Leu Asp Glu Leu Glu
 130 135 140
 Gln Ser Pro Ala Ser Tyr Gly Phe Pro Val Ala Leu Leu Gly Trp Ala
 145 150 155 160
 Met Met Gly Gly Ala Val Ala Val Leu Leu Gly Gly Gly Trp Gln Val
 165 170 175
 Ser Leu Ile Ala Phe Ile Thr Ala Phe Thr Ile Ile Ala Thr Thr Ser
 180 185 190
 Phe Leu Gly Lys Lys Gly Leu Pro Thr Phe Phe Gln Asn Val Val Gly
 195 200 205
 Gly Phe Ile Ala Thr Leu Pro Ala Ser Ile Ala Tyr Ser Leu Ala Leu
 210 215 220
 Gln Phe Gly Leu Glu Ile Lys Pro Ser Gln Ile Ile Ala Ser Gly Ile
 225 230 235 240
 Val Val Leu Leu Ala Gly Leu Thr Leu Val Gln Ser Leu Gln Asp Gly
 245 250 255
 Ile Thr Gly Ala Pro Val Thr Ala Ser Ala Arg Phe Phe Glu Thr Leu
 260 265 270
 Leu Phe Thr Gly Gly Ile Val Ala Gly Val Gly Leu Gly Ile Gln Leu
 275 280 285
 Ser Glu Ile Leu His Val Met Leu Pro Ala Met Glu Ser Ala Ala Ala
 290 295 300
 Pro Asn Tyr Ser Ser Thr Phe Ala Arg Ile Ile Ala Gly Gly Val Thr
 305 310 315 320
 Ala Ala Ala Phe Ala Val Gly Cys Tyr Ala Glu Trp Ser Ser Val Ile
 325 330 335
 Ile Ala Gly Leu Thr Ala Leu Met Gly Ser Ala Phe Tyr Tyr Leu Phe
 340 345 350
 Val Val Tyr Leu Gly Pro Val Ser Ala Ala Ala Ile Ala Ala Thr Ala
 355 360 365
 Val Gly Phe Thr Gly Gly Leu Leu Ala Arg Arg Phe Leu Ile Pro Pro
 370 375 380
 Leu Ile Val Ala Ile Ala Gly Ile Thr Pro Met Leu Pro Gly Leu Ala
 385 390 395 400
 Ile Tyr Arg Gly Met Tyr Ala Thr Leu Asn Asp Gln Thr Leu Met Gly
 405 410 415

Phe Thr Asn Ile Ala Val Ala Leu Ala Thr Ala Ser Ser Leu Ala Ala
 420 425 430

Gly Val Val Leu Gly Glu Trp Ile Ala Arg Arg Leu Arg Arg Pro Pro
 435 440 445

Arg Phe Asn Pro Tyr Arg Ala Phe Thr Lys Ala Asn Glu Phe Ser Phe
 450 455 460

Gln Glu Glu Ala Glu Gln Asn Gln Arg Arg Gln Arg Lys Arg Pro Lys
 465 470 475 480

Thr Asn Gln Arg Phe Gly Asn Lys Arg
 485

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<211> 440

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(417)

<223> RXS03183

<400> 1153

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Glu	Ala	Glu	Ala	Thr	Ala	Gly	Lys	Phe	Glu	Val	Gln	Pro	Leu	Val	Gly	
1	5							10						15		

aaa	gac	ggc	gtc	ggc	gta	tcc	acc	ctt	ggt	ggc	tac	aac	aac	ggc	atc	96
Lys	Asp	Gly	Val	Gly	Val	Ser	Thr	Leu	Gly	Gly	Tyr	Asn	Asn	Gly	Ile	
20	25							30								

aac	gtc	aac	tcc	gaa	aac	aag	gca	acc	gcc	cgc	gac	ttc	atc	gaa	ttc	144
Asn	Val	Asn	Ser	Glu	Asn	Lys	Ala	Thr	Ala	Arg	Asp	Phe	Ile	Glu	Phe	
35	40							45								

atc	atc	aac	gaa	gag	aac	caa	acc	tgg	tcc	gcg	gac	aac	tcc	ttc	cca	192
Ile	Ile	Asn	Glu	Asn	Gln	Thr	Trp	Phe	Ala	Asp	Asn	Ser	Phe	Pro		
50	55							60								

cca	gtt	ctg	gca	tcc	atc	tac	gat	gat	gag	tcc	ctt	gtt	gag	cag	tac	240
Pro	Val	Leu	Ala	Ser	Ile	Tyr	Asp	Asp	Glu	Ser	Leu	Val	Glu	Gln	Tyr	
65	70							75					80			

cca	tac	ctg	cca	gca	ctg	aag	gaa	tcc	ctg	gaa	aac	gca	gca	cca	cgc	288
Pro	Tyr	Leu	Pro	Ala	Leu	Lys	Glu	Ser	Leu	Glu	Asn	Ala	Ala	Pro	Arg	
85	90							95								

cca	gtg	tct	cct	ttc	tac	cca	gcc	atc	tcc	aag	gca	atc	cag	gac	aac	336
Pro	Val	Ser	Pro	Phe	Tyr	Pro	Ala	Ile	Ser	Lys	Ala	Ile	Gln	Asp	Asn	
100	105							110								

gcc	tac	gca	gcg	ctt	aac	ggc	aac	gtc	gac	gtt	gac	cag	gca	acc	acc	384
Ala	Tyr	Ala	Ala	Leu	Asn	Gly	Asn	Val	Asp	Val	Asp	Gln	Ala	Thr	Thr	
115	120							125								

gat atg aag gca gcg atc gaa aac gct tcc agc tagttcggtta atttagttca 437
 Asp Met Lys Ala Ala Ile Glu Asn Ala Ser Ser

130

135

ttc

440

<210> 1154

<211> 139

<212> PRT

<213> Corynebacterium glutamicum

<400> 1154

Glu	Ala	Glu	Ala	Thr	Ala	Gly	Lys	Phe	Glu	Val	Gln	Pro	Leu	Val	Gly
1															

5

10

15

Lys	Asp	Gly	Val	Gly	Val	Ser	Thr	Leu	Gly	Gly	Tyr	Asn	Asn	Gly	Ile

20

25

30

Asn	Val	Asn	Ser	Glu	Asn	Lys	Ala	Thr	Ala	Arg	Asp	Phe	Ile	Glu	Phe

35

40

45

Ile	Ile	Asn	Glu	Glu	Asn	Gln	Thr	Trp	Phe	Ala	Asp	Asn	Ser	Phe	Pro

50

55

60

Pro	Val	Leu	Ala	Ser	Ile	Tyr	Asp	Asp	Glu	Ser	Leu	Val	Glu	Gln	Tyr

65

70

75

80

Pro	Tyr	Leu	Pro	Ala	Leu	Lys	Glu	Ser	Leu	Glu	Asn	Ala	Ala	Pro	Arg

85

90

95

Pro	Val	Ser	Pro	Phe	Tyr	Pro	Ala	Ile	Ser	Lys	Ala	Ile	Gln	Asp	Asn

100

105

110

Ala	Tyr	Ala	Ala	Leu	Asn	Gly	Asn	Val	Asp	Val	Asp	Gln	Ala	Thr	Thr

115

120

125

Asp	Met	Lys	Ala	Ala	Ile	Glu	Asn	Ala	Ser	Ser					

130

135

<210> 1155

<211> 1212

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1189)

<223> RXC00874

<400> 1155

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tctggtttga tctcaccgc gatgaaaagg acgatatgga atg agc att ggc caa 115

Met Ser Ile Gly Gln

1

5

cac atc atc acc gag cgt ttc tac ggc gcc aag tcc cac acc atc gac 163

His Ile Ile Thr Glu Arg Phe Tyr Gly Ala Lys Ser His Thr Ile Asp

10

15

20

aac gta gat att gtg ttg tcc cgc gaa tgt ggc gag aac act ttg gct 211

Asn Val Asp Ile Val Leu Ser Arg Glu Cys Gly Glu Asn Thr Leu Ala			
25	30	35	
gta gtg cgc atc aac aat gcg ctg tat cag ttg ttg gtc aat gat gat			259
Val Val Arg Ile Asn Asn Ala Leu Tyr Gln Leu Leu Val Asn Asp Asp			
40	45	50	
ggc aaa gat gtt ctc aac gac cac gta gaa gag gtc ggt gcg agt ttc			307
Gly Lys Asp Val Leu Asn Asp His Val Glu Glu Val Gly Ala Ser Phe			
55	60	65	
gga gca tgg act ggc agc tct gct ttt ccc att ggc cct ttc act cca			355
Gly Ala Trp Thr Gly Ser Ser Ala Phe Pro Ile Gly Pro Phe Thr Pro			
70	75	80	85
ctc ggc aca gaa caa tcc aat agc tct ttc atc acc gcc gac aat aaa			403
Leu Gly Thr Glu Gln Ser Asn Ser Phe Ile Thr Ala Asp Asn Lys			
90	95	100	
gcg atc gtg aaa tac ttc cgc aaa tta gaa tcc ggg caa aac ccc gat			451
Ala Ile Val Lys Tyr Phe Arg Lys Leu Glu Ser Gly Gln Asn Pro Asp			
105	110	115	
gtg gag cta att tct aaa att tcc tcc tgc ccc aac atc gcg ccc atc			499
Val Glu Leu Ile Ser Lys Ile Ser Ser Cys Pro Asn Ile Ala Pro Ile			
120	125	130	
ctg ggt ttt tcc tcc gct gag atc tcc ggg gct aac tac acc ctg gtc			547
Leu Gly Phe Ser Ser Ala Glu Ile Ser Gly Ala Asn Tyr Thr Leu Val			
135	140	145	
atg gcg cag cag tac gtt cca ggt ttg gat ggc tgg tca cac gcg ctg			595
Met Ala Gln Gln Tyr Val Pro Gly Leu Asp Gly Trp Ser His Ala Leu			
150	155	160	165
act act acc tct ggc agc ttt gca gag gat gca gaa aag atc ggc gaa			643
Thr Thr Ser Gly Ser Phe Ala Glu Asp Ala Glu Lys Ile Gly Glu			
170	175	180	
gcc acc cgc aat gtt cac act gct ctt gca tcg gcc ttc cct act cgg			691
Ala Thr Arg Asn Val His Thr Ala Leu Ala Ser Ala Phe Pro Thr Arg			
185	190	195	
gta gtt ccc gta gaa gca ctc gcc gat gcg ctc act acc cgc ctt aat			739
Val Val Pro Val Glu Ala Leu Ala Asp Ala Leu Thr Thr Arg Leu Asn			
200	205	210	
gaa cta atc tcc caa gca ccc gaa atc gcc cgc ttc aaa gaa gca gcc			787
Glu Leu Ile Ser Gln Ala Pro Glu Ile Ala Arg Phe Lys Glu Ala Ala			
215.	220	225	
atc gac ctc tac caa tcg ttg gaa ggc gaa gcc cac atc caa cgc atc			835
Ile Asp Leu Tyr Gln Ser Leu Glu Gly Glu Ala His Ile Gln Arg Ile			
230	235	240	245
cac ggt gac ctc cac ttg ggg cag ctc atc aaa acc ccc gaa cgc tac			883
His Gly Asp Leu His Leu Gly Gln Leu Ile Lys Thr Pro Glu Arg Tyr			
250	255	260	
atc ctc atc gat ttc gaa ggc gaa cct gcc cgc cca ctt aat caa cga			931
Ile Leu Ile Asp Phe Glu Gly Glu Pro Ala Arg Pro Leu Asn Gln Arg			

265

270

275

cgc ctc ccc gac tct ccc ctg aaa gat ctc gcc ggc atc atc aga tcc 979
 Arg Leu Pro Asp Ser Pro Leu Lys Asp Leu Ala Gly Ile Ile Arg Ser
 280 285 290

atc gac tac gca gcc tac ttc gac ggc gaa cac acc caa tgg gcc aac 1027
 Ile Asp Tyr Ala Ala Tyr Phe Asp Gly Glu His Thr Gln Trp Ala Asn
 295 300 305

gaa gcc acc gcg cta ttc ctc gac ggc tac gga tca att gaa gac caa 1075
 Glu Ala Thr Ala Leu Phe Leu Asp Gly Tyr Gly Ser Ile Glu Asp Gln
 310 315 320 325

gaa ctc ctc aat gcc tac att ctg gac aag gcg ttg tac gag gtt gcc 1123
 Glu Leu Leu Asn Ala Tyr Ile Leu Asp Lys Ala Leu Tyr Glu Val Ala
 330 335 340

tat gaa ata aac aac cgc ccc gac tgg gtg aaa atc cca ctc gag gcg 1171
 Tyr Glu Ile Asn Asn Arg Pro Asp Trp Val Lys Ile Pro Leu Glu Ala
 345 350 355

gtc gaa agg ctt cta gac tagtttagtta ctctgcgtca aac 1212
 Val Glu Arg Leu Leu Asp
 360

<210> 1156

<211> 363

<212> PRT

<213> Corynebacterium glutamicum

<400> 1156

Met Ser Ile Gly Gln His Ile Ile Thr Glu Arg Phe Tyr Gly Ala Lys
 1 5 10 15

Ser His Thr Ile Asp Asn Val Asp Ile Val Leu Ser Arg Glu Cys Gly
 20 25 30

Glu Asn Thr Leu Ala Val Val Arg Ile Asn Asn Ala Leu Tyr Gln Leu
 35 40 45

Leu Val Asn Asp Asp Gly Lys Asp Val Leu Asn Asp His Val Glu Glu
 50 55 60

Val Gly Ala Ser Phe Gly Ala Trp Thr Gly Ser Ser Ala Phe Pro Ile
 65 70 75 80

Gly Pro Phe Thr Pro Leu Gly Thr Glu Gln Ser Asn Ser Ser Phe Ile
 85 90 95

Thr Ala Asp Asn Lys Ala Ile Val Lys Tyr Phe Arg Lys Leu Glu Ser
 100 105 110

Gly Gln Asn Pro Asp Val Glu Leu Ile Ser Lys Ile Ser Ser Cys Pro
 115 120 125

Asn Ile Ala Pro Ile Leu Gly Phe Ser Ser Ala Glu Ile Ser Gly Ala
130 135 140

Asn Tyr Thr Leu Val Met Ala Gln Gln Tyr Val Pro Gly Leu Asp Gly
145 150 155 160

Trp Ser His Ala Leu Thr Thr Ser Gly Ser Phe Ala Glu Asp Ala
165 170 175

Glu Lys Ile Gly Glu Ala Thr Arg Asn Val His Thr Ala Leu Ala Ser
180 185 190

Ala Phe Pro Thr Arg Val Val Pro Val Glu Ala Leu Ala Asp Ala Leu
195 200 205

Thr Thr Arg Leu Asn Glu Leu Ile Ser Gln Ala Pro Glu Ile Ala Arg
210 215 220

Phe Lys Glu Ala Ala Ile Asp Leu Tyr Gln Ser Leu Glu Gly Glu Ala
225 230 235 240

His Ile Gln Arg Ile His Gly Asp Leu His Leu Gly Gln Leu Ile Lys
245 250 255

Thr Pro Glu Arg Tyr Ile Leu Ile Asp Phe Glu Gly Glu Pro Ala Arg
260 265 270

Pro Leu Asn Gln Arg Arg Leu Pro Asp Ser Pro Leu Lys Asp Leu Ala
275 280 285

Gly Ile Ile Arg Ser Ile Asp Tyr Ala Ala Tyr Phe Asp Gly Glu His
290 295 300

Thr Gln Trp Ala Asn Glu Ala Thr Ala Leu Phe Leu Asp Gly Tyr Gly
305 310 315 320

Ser Ile Glu Asp Gln Glu Leu Leu Asn Ala Tyr Ile Leu Asp Lys Ala
325 330 335

Leu Tyr Glu Val Ala Tyr Glu Ile Asn Asn Arg Pro Asp Trp Val Lys
340 345 350

Ile Pro Leu Glu Ala Val Glu Arg Leu Leu Asp
355 360